

From: Chan, Christina
Sent: Friday, February 17, 2006 9:09 AM
To: Sitton, Jehanne Souaya; STIC-Biotech/CheMlib
Subject: RE: rush search for an after final

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
FEB 17 2006
...
(STIC)

-----Original Message-----

From: Sitton, Jehanne Souaya
Sent: Friday, February 17, 2006 8:05 AM
To: Chan, Christina
Subject: rush search for an after final

Christina,
Please forward this rush request to STIC. It's for an afterfinal.

Please perform an interference search for the following: 1) nucleotides 1-1407 of SEQ ID NO: 1 and 2) nucleotides 11200-12800 for SEQ ID NO: 1 in application 09/673,476.

*Up this is a mistake - Stic
searched 1533 base pairs
from position 11199 -
12732
of Seq 1*

thanks,
Jehanne Sitton
Primary Examiner
Art Unit 1634
Rem-2D81 (office)
Rem-2C70 (mailbox)
571-272-0752

Searcher: Noble
Searcher Phone: _____
Date Searcher Picked up: 2/17/06
Date completed: 2/21/06
Searcher Prep Time: 5
Online Time: 5

Type of Search
NA# 2 AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: compugen
WWW/Internet: _____
Other (Specify): _____

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OM nucleic - nucleic search, using sw model.

Run on: February 19, 2006, 20:22:54 ; Search time 284.179 Seconds (without alignments)

9589.048 Million cell updates/sec

Title: US-09-673-476-1_COPY_11200_12800

Perfect score: 1533

Sequence: atgttcagtcgcgaaacctc.....gtcggtgtggctggctcg 1533

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/1 COMB .seq:*
 2: /cgn2_6/ptodata/1/ina/5 _COMB .seq:*
 3: /cgn2_6/ptodata/1/ina/6A COMB .seq:*
 4: /cgn2_6/ptodata/1/ina/6B COMB .seq:*
 5: /cgn2_6/ptodata/1/ina/H COMB .seq:*
 6: /cgn2_6/ptodata/1/ina/PCTUS COMB .seq:*
 7: /cgn2_6/ptodata/1/ina/P COMB .seq:*
 8: /cgn2_6/ptodata/1/ina/RE COMB .seq:*
 9: /cgn2_6/ptodata/1/ina/backfiles.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153.3	100.0	12732	3 US-09-060-756-1	Sequence 1, Appli
2	153.3	100.0	12732	3 US-09-060-756-1	Sequence 1, Appli
3	153.3	100.0	440765	3 US-09-060-756-1	X Sequence 2, Appli
4	153.3	100.0	441529	3 US-09-060-756-1	Sequence 1, Appli
c 5	111.9	73.0	1119	3 US-09-060-756-1	Sequence 53, Appli
c 6	479.8	311.2	440765	3 US-09-060-756-1	Sequence 2, Appli
c 7	478.2	311.2	441529	3 US-09-060-756-1	Sequence 1, Appli
c 8	311.2	20.3	894	3 US-09-060-756-1	Sequence 52, Appli
c 9	56	3.7	1236	3 US-09-060-756-1	Sequence 127, Appli
c 10	56	3.7	1232	3 US-09-060-756-1	Sequence 2466, Appli
c 11	56	3.7	14077	3 US-09-060-756-1	Sequence 1109, Appli
c 12	54.4	3.5	9521	3 US-09-060-756-1	Sequence 953, Appli
c 13	53	3.5	2067	2 US-09-060-756-1	Sequence 8, Appli
c 14	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 15	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 16	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 17	53	3.5	2155	3 US-09-060-756-1	Sequence 30, Appli
c 18	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 19	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 20	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 21	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 22	51.8	3.4	58857	3 US-09-060-756-1	Sequence 1, Appli
c 23	51.6	3.4	12449	3 US-09-060-756-1	Sequence 15755, Appli
c 24	50.8	3.3	1344	3 US-09-060-756-1	Sequence 9345, Appli

ALIGNMENTS

RESULT 1
US-09-060-756-1

; Sequence 1, Application US/09060756

; Patent No. 6183957

; GENERAL INFORMATION:

; APPLICANT: Cole, Stewart

; APPLICANT: Buchrisser-Brosch, Roland

; APPLICANT: Gordon, Stephen

; APPLICANT: Billault, Alain

; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

; FILE REFERENCE: 3495-0169

CURRENT APPLICATION NUMBER: US/09/060-756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 12732

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

US-09-060-756-1

Result No.	Score	Query Match	Length	DB ID	Description
1	153.3	100.0	12732	3 US-09-060-756-1	Sequence 1, Appli
2	153.3	100.0	12732	3 US-09-060-756-1	Sequence 1, Appli
3	153.3	100.0	440765	3 US-09-060-756-1	X Sequence 2, Appli
4	153.3	100.0	441529	3 US-09-060-756-1	Sequence 1, Appli
c 5	111.9	73.0	1119	3 US-09-060-756-1	Sequence 53, Appli
c 6	479.8	311.2	440765	3 US-09-060-756-1	Sequence 2, Appli
c 7	478.2	311.2	441529	3 US-09-060-756-1	Sequence 1, Appli
c 8	311.2	20.3	894	3 US-09-060-756-1	Sequence 52, Appli
c 9	56	3.7	1236	3 US-09-060-756-1	Sequence 127, Appli
c 10	56	3.7	1232	3 US-09-060-756-1	Sequence 2466, Appli
c 11	56	3.7	14077	3 US-09-060-756-1	Sequence 1109, Appli
c 12	54.4	3.5	9521	3 US-09-060-756-1	Sequence 953, Appli
c 13	53	3.5	2067	2 US-09-060-756-1	Sequence 8, Appli
c 14	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 15	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 16	53	3.5	2155	3 US-09-060-756-1	Sequence 4, Appli
c 17	53	3.5	2155	3 US-09-060-756-1	Sequence 30, Appli
c 18	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 19	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 20	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 21	53	3.5	6200	3 US-09-060-756-1	Sequence 1, Appli
c 22	51.8	3.4	58857	3 US-09-060-756-1	Sequence 1, Appli
c 23	51.6	3.4	12449	3 US-09-060-756-1	Sequence 15755, Appli
c 24	50.8	3.3	1344	3 US-09-060-756-1	Sequence 9345, Appli

Qy	481	TTCCTGGCGGCCGCCCCCTGGCGCCGAGCTGGACGTTGGCATCTGGCAAGATGCC	540
Db	11680	TTCCTGGCGGCCGCCCCCTGGCGCCGAGCTGGCATCTGGCAAGATGCC	11739
Qy	541	AGTGGCCTAATGAGCTGGATGAGCTCTGGCGGCCGAGCTGGCATCTGGCAAGATGCC	600
Db	11740	AGTGGCCTAATGAGCTGGATGAGCTCTGGCGGCCGAGCTGGCATCTGGCAAGATGCC	11799
Qy	601	TCCGGTCAAACTGTGGCATGGCCGACCCCTGGTCAACCAGAACCTTGCGGTTCCA	660
Db	11880	TCCGGTCAAACTGTGGCATGGCCGACCCCTGGTCAACCAGAACCTTGCGGTTCCA	11859
Qy	661	CCACTGGTTGGCACANGCTTGGCTGGCGGATACGGCATCTGGTGGCA	720
Db	11860	CCACTGGTTGGCACANGCTTGGCTGGCGGATACGGCATCTGGTGGCA	11919
Qy	721	ACATGGCATGTGCCCATTGACCCGGTGGGAAGTGTAGATAACCGTCAAGGGCATGTA	780
Db	11920	ACATGGCATGTGCCCATTGACCCGGTGGGAAGTGTAGATAACCGTCAAGGGCATGTA	11979
Qy	781	CCTGGGCGGAAATGTCGTGTAGGGCTCAGGGCAGGTACGGCCAGTTGGCTGGGA	840
Db	11980	CCTGGGCGGAAATGTCGTGTAGGGCTCAGGGCAGGTACGGCCAGTTGGCTGGGA	12039
Qy	841	TGAGTTATCAGATCAACGATTGGCTCAAGGTCAAGTGGCATCTGGGATGAAAGCACA	900
Db	12040	TGAGTTATCAGATCAACGATTGGCTCAAGGTCAAGTGGCATCTGGGATGAAAGCACA	12099
Qy	901	ACTTCGACTCTTGGCATGGCGCTCCTCCATATCACTCGACCGATGAAAGCACA	960
Db	12100	ACTTCGACTCTTGGCATGGCGCTCCTCCATATCACTCGACGGATGAAAGCACA	12159
Qy	961	TGCTCTTGGGGTGCCTGGGATGCGGACTGCTGGTTGCTTAGCTTCAAGGGATCTCAT	1020
Db	12160	TGCTCTTGGGGTGCCTGGGATGCGGACTGCTGGTTGCTTAGCTTCAAGGGATCTCAT	12219
Qy	1021	AGTAGTCTCCGGCTCGAACCGGACGCTACTCCGGCGAGGGCCGACAGGGGCCGG	1080
Db	12220	AGTAGTCTCCGGCTCGAACCGGACGCTACTCCGGCGAGGGCCGACAGGGGCCGG	12279
Qy	1081	TCAAGGTTCCCATGAGGGCGAGGTTTTCGGTCTCGAACATGGCGGAAACACGCTGGGGT	1140
Db	12280	TCAAGGTTCCCATGAGGGCGAGGTTTTCGGTCTCGAACATGGCGGAAACACGCTGGGGT	12339
Qy	1141	ACGGCTCGCGCTTAATCAACGATGATGCCCGGGGGTGCATGGTCAAGGCTCTGGCGA	1200
Db	12340	ACGGCTCGCGCTTAATCAACGATGATGCCCGGGGGTGCATGGTCAAGGCTCTGGCGA	12399
Qy	1201	CGATGATCTCCACCGGAAAGTCGGTTGGCTGAGAAGCTGGCTGAGGCTGAGGG	1260
Db	12400	CGATGATCTCCACCGGAAAGTCGGTTGGCTGAGAAGCTGGCTGAGGCTGAGGG	12459
Qy	1261	CGTAGGCCGGCTGGTTGGCTGAGGAGCTCACCTGGGGCAAGCTGGGAC	1320
Db	12460	CGTAGGCCGGCTGGTTGGCTGAGGAGCTCACCTGGGGCAAGCTGGGAC	12519
Qy	1321	TCAAGGTTCCCTTTCCTGGCGCCAGGTTTTCGGTCTGGCAAGTGGATCGC	1380
Db	12520	TCAAGGTTCCCTTTCCTGGCGCCAGGTTTTCGGTCTGGCAAGTGGATCGC	12579
Qy	1381	CTGTGCCCCGGCGTGGCGCTGGCTGGCTGGCTGGCGACGTTGGCAAGCTGGCT	1440
Db	12580	CTGTGCCCCGGCGTGGCGCTGGCTGGCTGGCGACGTTGGCAAGCTGGCT	12639
Qy	1441	GGGAAGTATGAGCTGGGCTGGTGGCACTGGCTGGGGCTGGTGGGG	1500
Db	12640	GGGAAGTATGAGCTGGGCTGGTGGCACTGGCTGGGGCTGGTGGGG	12699
Qy	1501	CGCACCGTCTCGAGTGGCTGGCTGGCTGGCTGC	1533
Db	12700	CGCACCGTCTCGAGTGGCTGGCTGGCTGC	12732

```

; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

Query Match          100.0%; Score 1533; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1533; Conservative 0; Pairs 0; Gaps 0;

Qy          1 ATGTTCAAGTCGGCAACCTCGATCCGAGAACCTGAATTCCCATGCGCGAACCCGAC 60
Db          1707214 ATGTCAGGTGGCAACCTCGATCCGAGAACCTGAATTCCCATGCGCGAACCCGAC 1707273
Qy          61 GCGTACCCGCCTTCCAAGAGGCCACATGCCGAACTCCGAGACTGCTGCTCTGTCGCCGAA 120
Db          1707274 GCGTACCCGCCTTCCAAGAGGCCACATGCCGAACTCCGAGACTGCTGCTCTGTCGCCGAA 1707333
Qy          121 AAGAGGGTTTCCAGAATCCCGCGCCAGATAACCCAGAGCATTCTCTTAACGTGGCG 180
Db          1707334 AAGAGGGTTTCCAGAATCCCGCGCCAGATAACCCAGAGCATTCTCTTAACGTGGCG 1707393
Qy          181 GAGAACTCGGATCTGCAAGGTTCTCGTGTGTCAGGGAACTGTTGTCGGGGTGAATTG 240
Db          1707394 GAGAACTCGGATCTGCAAGGTTCTCGTGTGTCAGGGAACTGTTGTCGGGGTGAATTG 1707453
Qy          241 ACCGGCGCCGCCGAAATGTTCTGCAATCACTTGTGTAGCCCTTCCGCTGCTGG 300
Db          1707454 ACCGGCGCCGCCGAAATGTTCTGCAATCACTTGTGTAGCCCTTCCGCTGCTGG 1707513
Qy          301 TTTCCTGCAATGGTCAAGGTCTGGAGCGCCGGCTGGAGCGGGCAACATCCACAG 360
Db          1707514 TTTCCTGCAATGGTCAAGGTCTGGAGCGCCGGCTGGAGCGGGCAACATCCACAG 1707573
Qy          361 GCCCCCTGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 420
Db          1707574 GCCCCCTGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707633
Qy          421 CGGGTGTCCGCCCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 480
Db          1707634 CGGGTGTCCGCCCGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707693
Qy          481 TTTCCTGCGCGCGCCGCCCTCGCGGCCCTGGAAACGTTGGCATGGCGAAGGGATC 540
Db          1707694 TTTCCTGCGCGCGCCGCCCTCGCGGCCCTGGAAACGTTGGCATGGCGAAGGGATC 1707753
Qy          541 AGTGCGCTATGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 600
Db          1707754 AGTGCGCTATGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707813
Qy          601 TCGCTCAACGTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 660
Db          1707814 TCGCTCAACGTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707873
Qy          661 CCACCTGGTTGTCGCAATGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 720
Db          1707874 CCACCTGGTTGTCGCAATGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707933
Qy          721 ACATGGCTGGTGTGCCATGACCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 780
Db          1707934 ACATGGCTGGTGTGCCATGACCCCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1707993
Qy          781 CGTCGGCACGAATGTCGCTGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 840
Db          1707994 CGTCGGCACGAATGTCGCTGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1708053
Qy          841 TGAAGTTCATCAAGTCAACGTCATGCCCTGAAGTCAAGTCAACGTCATGCCCTGA 900

```


RESULT 6
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
; Patent No. 6294328
GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; WHITE, Owen R.
; ADDRESS: 24366-20007.00
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match Score 479.8 ; DB 3 ; Length 4403765;
Best Local Similarity 71.6% ; Pred. No. 1.3e-94 ;
Matches 644 ; Conservative 0 ; Mismatches 252 ; Indels 3 ; Gaps 1 ;

Query 412 GCGCCGCCGCGGGTGTGCCACGGCCAGCATGGCATTCCGGATGGC 471
Db 17112040 GCGCAGGGCTTGGCCACCGGGTTAGACAGATCGTATCCGGATGGT 1711981
Query 472 GCGCGATGGTTCTGTGAGCCGGGCCCTCCGGGCGGATGGGATCTGGC 531
Db 1711980 CGCGATGGACTTCAGAGCACGGCGACCCCTGTCGGCGG 1711921
Query 532 GAAAGTCACTGGCATATGGGATGCTGGATGCTTCGGCGGAGACA 591
Db 1711920 GAAGCCCCGGGACACTTCAGCGATGCTTCGGCGGCTGGACTA 1711861
Query 592 GTTGGACATCGTCAAACCTGGCCATGCCGACCCCTGGCTAACAGAACCTTG 651
Db 1711860 GTTGGACATCGTCAAACCTGGCCATGCCGACCCCTGGCTAACAGAACCTTG 1711801
Query 652 GCGGGTCCACCACTCTGGTGCACATGGCTGGCGATACGGCCATGG 711
Db 1711800 GCGGGTCACTGTAGCTGGGAATCCAATGGCTGGCACTGAGCCATCG 1711741
Query 712 TGTGGCCAACTGGCAATGGCTAACATGGCTGGGATGAGGTGGCT 771
Db 1711740 TCTGGCCAACTGGCTGGCAATGGCTGGGATGAGGTGGCT 1711681
Query 772 GGGCATGACCTGGCAGGAATGTCGTCGAGGGGAGCTGGCCAGT 831
Db 1711680 TCGCATGACCTGGCAGGAATGTCGTCGAGGGGAGCTGGCCAGT 1711621
Query 832 TGTGCTGGATGAATTCAAGATCAAGCTGGCTGGGATGCTGGCT 891
Db 1711620 TGTGCTGGATGAATTCAAGCTGGCTGGGAGCTGGCTGGGAGCTGA 1711561
Query 892 CGGGGGAACTTGAGCTGGCTGGGAAATGGCTGGGAGCTGGCTGGGAGCTGA 951

RESULT 7
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
; Patent No. 6294328
GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; ADDRESS: 24366-20007.00
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match Score 478.2 ; DB 3 ; Length 4411529;
Best Local Similarity 71.5% ; Pred. No. 2.8e-94 ;
Matches 633 ; Conservative 0 ; Mismatches 253 ; Indels 3 ; Gaps 1 ;

Query 412 GCGCCGCCGCGGGTGTGCCACGGCCAGCATGGCATTCCGGATGGC 471
Db 1711911 GCGCAGGGCTTGGCCACCGGGTGTGCGCCATGGGATGGT 1711852
Query 472 GCGGATGGTTCTGTGAGCCGGGCCCTCCGGGCGGATGGGATCTGGC 531
Db 1711851 CGCGATGGACTTCAGAGCACGGGGCATGGCTCCGGGAGCTGGC 1711792
Query 532 GAAAGTCACTGGCATATGGGATGCTGGATGCTTCGGCGGAGACA 591
Db 1711791 GAAGCCCCGGGACACTTCAGCGATGCTTCGGCGGAGACA 1711732
Query 592 GCGGATGGCTGGCTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGGC 651
Db 1711731 GTGAGGGTCACTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGGC 1711672
Query 652 CGGGGTCCACCACTCTGGTGCACATGGCTGGGATGAGGTGGCT 771
Db 1711670 CGGGGTCCACCACTCTGGTGCACATGGCTGGGATGAGGTGGCT 1711621

Qy 712 TGTGGGAAACATCGGATGTCGATCGACCCGGACTGCAAGTACAGTCCA 771
 Db 1711611 TCTGGGAAACATCGGATCTCGGATCGGATCGGATCGAATCTA 1711552
 Qy 772 GGGCATGAGCTCGGAGGAATGTCGCTGAGGGGAGCTAACGGGAGT 831
 Db 1711551 TCGCATGAGCTCGGAGGAATGTCGCTGAGGGGAGCTAACGGGAGT 1711492
 Qy 832 TGGCTGATGAGTTCAAGATTAAGCCTAACGATTCAGTTGCCGCCAGAA 891
 Db 1711491 TGGTTGGATGAGCTCCGGAGGCAATTCAGGTGCGCTGAGTGA 1711432
 Qy 892 CGGGGGAAACTCGAGTCTTGCAATGGCTGGCATCGACGGGATGAA 951
 Db 1711431 GCGCGGGAAACTCGAGTCTTGCAATGGCTGGCATCGACGGGATGAA 1711375
 Qy 952 AGCACACCCCTCGTGTGGCTGGGGATGGCAACTTGTCTAGCTCAC 1011
 Db 1711374 AACACACCGTCGTCGGATCGGGTCAAGGTACTTACCTGCTGAA 1711315
 Qy 1012 GATGATCCAGTAGTCGCGCTCGGAGCTACTGGCGGGCCGACA 1071
 Db 1711314 GATGGTCAGTAACTGCGCTTCGCAAGTCGAGCTGGCGGACA 1711255
 Qy 1072 GGGGGCGCTCAAGTCCATTGGGGAGTTTCGTCGAAATGGGGAGA 1131
 Db 1711254 GCACATCCTGAAATTGGCGTGGACCGATGGGTTGCCCCAGATGGCGGAA 1711195
 Qy 1132 CGTCCGGGATACCGCTCGGGTACTACGGATGTCGCGGGGCTGCGGT 1191
 Db 1711194 GCTCGGATAGCGGGGTACTCTCTATGATCGGCGGCAT 1711135
 Qy 1192 CGTCCGGGATACCGCTCGGGTACTACGGATGTCGCGGGGCTGCGGT 1251
 Db 1711134 CGTCAGCGATGATCACCTCGACGGGAACTCGTCCCTGGGG 17111075
 Qy 1252 CCTGACGGCGGTAGCCGGCTGGTGTGAGTCGAGCTGGGGAA 1310
 Db 1711074 CCTGGCGGATGTACTCCTTGAGTGGAGATCGAGCTACCTGGCGAA 1711016

RESULT 8
 US-09-894-844-52/c
 Sequence 52; Application US/0984844
 Patent No. 6685156
 GENERAL INFORMATION:
 APPLICANT: Behr, Marcel
 APPLICANT: Small, Peter
 APPLICANT: Schoonink, Gary A.
 APPLICANT: Wilson, Michael A.
 TITLE OF INVENTION: Molecular Differences Between Species of
 the M. tuberculosis Complex
 FILE REFERENCE: STAN102CON
 CURRENT APPLICATION NUMBER: US/09/894,844
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: 09/318,191
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: 60/097,936
 PRIOR FILING DATE: 1998-08-25
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO: 52
 LENGTH: 894
 ORGANISM: Mycobacteria tuberculosis
 US-09-894-844-52

Query Match 20.3%; Score 311; DB 3; Length 894;
 Best Local Similarity 100.0%; Pred. No. 1.7e-38;
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.3%; Score 311; DB 3; Length 1236;
 Best Local Similarity 62.2%; Pred. No. 0.005;
 Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1348 CGCAAAGGTATGGGATGGCGGAACTGGCTGGCCGGCGGT 1407
 Db 1062 CGCTGGCTGGAGTACGGCTGGCGGCGGTACGGCTGGCCGGCG 1003
 Db 1062 CGCTGGCTGGAGTACGGCTGGCGGCGGTACGGCTGGCCGGCG 1407
 Qy 1408 GGCTGGCTGGGGAGCTACGGCTGGCGGAACTGGCTGGCCGGCG 1467
 Db 1002 GGCTGGCTGGGGAGCTACGGCTGGCCGGCGGTACGGCTGGCCGG 943
 Qy 1468 GTTGGGGCTGGAAACCGC 1483
 Db 942 GTTGGCTGGAAACCGC 927

RESULT 10
 US-09-902-540-2466/c
 Sequence 2466; Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.

Qy * 1 ATGTCAGCTCGGAAACCTCGATCCCGAGGACTCTGAATCCCATGCGGAAACCCGAC 60

Page 8

Myxococcus xanthus Genome Sequences and Uses Thereof						
RESULT 11 US-09-902-540-1109						
APPLICANT: Hinkle, Gregory J.						
APPLICANT: Slater, Steven C.						
APPLICANT: Wiegand, Roger C.						
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof						
FILE REFERENCE: 38-10(15849) B						
CURRENT APPLICATION NUMBER: US/09/902,540						
CURRENT FILING DATE: 2001-07-10						
PRIOR APPLICATION NUMBER: 60/217,883						
PRIOR FILING DATE: 2000-07-10						
NUMBER OF SEQ ID NOS: 16825						
SEQ ID NO: 2466						
LENGTH: 1574						
TYPE: DNA						
ORGANISM: Myxococcus xanthus						
US-09-902-540-2466						
Query Match Score 56 ; DB 3 ; Length 1574 ;						
Best Local Similarity 4.1% ; Pred. No. 0.0052 ; Mismatches 265 ; Indels 6 ; Gaps Matches 241 ; Conservative 0 ;						
Qy 355 CCAAGGCCCTGGGTCGGCTCGCCGAGCTTGCCACTGGCTTGAGCC 4						
Db 1224 CCACCCGGCTTCCGGGCTTCATGTGCGCATGACCTGGCTGG 1						
Qy 415 GCGCGCCGGTGTGCGCCGGTGTGCGAGGATGGATTCGGGATGGCG 4						
Db 1169 GAGGCGGATCAACCCGGGTG-GGTCTGTCACGGGATCAGGGT 1						
Qy 475 CGATGGTTTCCCTGAGCGCGGCCCTGGGCTTGAAACCTGGGATCTGG 5						
Db 1110 TGAAGGCCTGGGCAATGGGGGGCTGGCTGGCATGGGCTGTGG 1						
Qy 535 GAAATCCAGTGGCATGAGGGATGAGTCTCGCGGGGCTCCGGGACAGGT 5						
Db 1050 CGTTCGAGGCCCTCATGAGGGCCACCTTGTCAAGGGCTCTGGCT 9						
Qy 595 CGAGCATGGTCAAACCTGGCCATGCCCGAACCCCTCGTAACCGAACCTGGGG 6						
Db 990 CGGAGGCGGAGCGCCGAGCGCCGCACTAGAGGGCCCTTCAGGGGGCG 9						
Qy 655 GTTCCACACCCPRTGGTGTGGCACATGCCCTGGGCTGGGGATAACAGCGCATGGT 7						
Db 930 GAGGACCGGCTGTGCGAGGCCAGGGCCATGGGGCTTCAGGGGGGGGGGG 8						
Qy 715 CGGGCAAATGGGATGTGCCATGACCGGCTGGCATACCGTCAGGG 7						
Db 870 GGTCCACATCCATGACCTTGTAGGAGGCCCTGGGCTGAGGTAGGCCACATCATGG 8						
Qy 775 GGTGAGCTGGGAGGAATGTCGCTGAGCTGGGAGCGGTACACGGCGAGTTGG 8						
Db 810 AGAAGGTGTCCTGGGGGATGAGCCGTACCGGCCCTGGGCTGG 7						
Qy 835 TCTGGGAGAAGTTCATCGAGATAACGCAATCC 866						
Db 750 GCAAGGAGAGCTGACGCCGTTGACGGCCACCC 719						
APPLICANT: Hinkle, Barry S.						
APPLICANT: Goldman, Barry S.						
APPLICANT: Hinkle, Gregory J.						
APPLICANT: Slater, Steven C.						
APPLICANT: Wiegand, Roger C.						
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof						
FILE REFERENCE: 38-10(15849) B						
CURRENT APPLICATION NUMBER: US/09/902,540						
CURRENT FILING DATE: 2001-07-10						
PRIOR APPLICATION NUMBER: 60/217,883						
PRIOR FILING DATE: 2000-07-10						
NUMBER OF SEQ ID NOS: 16825						

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 89...2047
S-09-385-707-4

Search completed: February 19, 2006, 20:42:30
Search time: 309.179 secs

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OM nucleic - nucleic search, using SW model

Run on: February 20, 2006, 01:31:10 ; Search time 1317.13 Seconds
(without alignments)

9624.692 Million cell updates/sec

Title: US-09-673-476-1_COPY_11200_12800

Perfect score: 1533

Sequence: 1 atgttcagtctcgagaacctc.....gtcgatgtttggctcg 1533

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 Summaries

Database : Published Applications NA Main:*
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10: /cgn2_6/ptodata/1/pubnra/US11_PUBCOMB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	153.3	100.0	12732	6	US-10-259-678-1	X	Sequence 1, Appli
c 2	112.2	73.2	1122	7	US-10-282-122A-28775		Sequence 28775, A
c 3	111.9	73.0	1119	3	US-09-894-844-53		Sequence 53, Appli
c 4	111.9	73.0	1119	7	US-10-388-902-53		Sequence 53, Appli
c 5	111.9	73.0	1119	7	US-10-647-089-53		Sequence 53, Appli
c 6	479.8	31.3	1074	7	US-10-282-122A-28776		Sequence 28776, A
c 7	415.2	27.1	1074	7	US-10-282-122A-25331		Sequence 25931, A
c 8	311	20.3	894	3	US-09-884-844-52		Sequence 52, Appli
c 9	311	20.3	894	7	US-10-388-902-52		Sequence 52, Appli
c 10	311	20.3	894	7	US-10-647-089-127		Sequence 52, Appli
c 11	194.4	12.7	366	7	US-10-282-122A-26084		Sequence 26084, A
c 12	104.8	6.8	276	7	US-10-282-122A-25902		Sequence 25902, A
c 13	72.8	4.7	951	7	US-10-282-122A-13587		Sequence 13587, A
c 14	65.2	4.3	1395	3	US-10-282-122A-35893		Sequence 35893, A
c 15	57.4	3.7	884.2	3	US-09-9176-059-1		Sequence 1, Appli
c 16	56	3.7	1236	3	US-09-894-844-127		Sequence 127, APP
c 17	56	3.7	1236	7	US-10-388-902-127		Sequence 127, APP
c 18	56	3.7	1236	7	US-10-647-089-127		Sequence 127, APP
c 19	56	3.7	1236	8	US-10-481-265-6		Sequence 6, Appli
c 20	55.6	3.6	1544	7	US-10-417-963-7661		Sequence 7661, AP
c 21	54.2	3.6	2196	6	US-10-349-021-11		Sequence 5077, AP
c 22	54.8	3.6	2196	6	US-10-156-761-5077		Sequence 5077, AP
c 23	54.8	3.6	2517	7	US-10-282-122A-25466		Sequence 25466, A

RESULT 1
US-10-259-678-1

; Sequence 1, Application US/10259678
; Publication No. US20030198974A1
; GENERAL INFORMATION:
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Cole, Stewart
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/10/259,678
; PRIORITY APPLICATION NUMBER: US/09/060,756
; PRIORITY FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 12732
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-10-259-678-1

Query Match 100.0%; Score 1533; DB 6; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAGCTCCGAATCCCATGCCGAGCTGAAATCCGTGGACCGCCGAGCCGACC 60
Db 11200 ATGTTAGCTCCGAATCCCATGCCGAGCTGAAATCCGTGGACCGCCGAGCCGACC 11259
QY 61 GGCTAACCCGCCCTTCAGCAAGCAGCATGGCCTAGGTGGCTTGTCCCCGGGA 120
Db 11260 GGCTAACCCGCCCTTCAGCAAGCAGCATGGCCTAGGTGGCTTGTCCCCGGGA 11319
QY 121 AGACCGTTCCAGAATTCGCGAGATGAACTGGGAGATGGCTAACGTGGCGC 180
Db 11320 AGACCGTTCCAGAATTCGCGAGATGGCTAACGTGGCGC 11379
QY 181 GAGGATCTCGGTPATCGTCAAAGTTCCTGTGAACTGGGAACTGGCTGAATTGT 240
Db 11380 GAGGATCTCGGTPATCGTCAAAGTTCCTGTGAACTGGGAACTGGCTGAATTGT 11439
QY 241 ACCGGCGGGCGGCGAATGTTCCGTGGCATCATCTGGTTAGCCCTTGCTCTGGGG 300

Publication No. US20040061923A1	Qy	977 GTCGAGGAAATGACCTCGTGTGCTTAGTTCAAGGATCATCCAGTCGGTACGTCGGCTCTC 1036
GENERAL INFORMATION:		
APPLICANT: Behr, Marcel	Db	459 GTCAGAGAATGACCTCGTGTGCTTAGTTCAAGGATCATCCAGTCGGTACGTCGGCTCTC 400
APPLICANT: Small, Peter		
APPLICANT: Schoonik, Michael A.	Qy	1.037 GCACAAAGGAACTCGACTCGCGAGCGGGCGAGCGGGCGATCCATTGAG 1096
APPLICANT: Wilson, Michael A.	Db	399 GCACAAAGGAACTCGACTCGCGAGCGGGCGAGCGGGCGATCCATTGAG 340
TITLE OF INVENTION: Molecular Differences Between Species of	Qy	
FILE REFERENCE: STAN102CON	Db	
CURRENT APPLICATION NUMBER: US10/647,089	Qy	1.097 GCCGAGGTTTCGTTCTGAAGATGGCGGAACACGTCGGGATACGGCTGGCTACTC 1156
PRIOR APPLICATION NUMBER: US09/894,844	Db	339 GCCGAGGTTTCGTTCTGAAGATGGCGGAACACGTCGGGATACGGCTGGCTACTC 280
PRIOR FILING DATE: 2001-06-27	Qy	1.157 AGGATGATGCGCGGGATGGCATGGTCACGCGTGCGAGATGATCTCACCGG 1216
PRIOR APPLICATION NUMBER: 09/318,191	Db	279 AGGATGATGCGCGGGATGGCATGGTCACGCGTGCGAGATGATCTCACCGG 220
PRIOR FILING DATE: 1999-05-25	Qy	1.217 GAACTCGGTTTCGTCGAGGATGCTGAAAGCTGTCGAAGGGCTAGSCCGCTGGT 1276
PRIOR APPLICATION NUMBER: 60/097,936	Db	219 GAACTCGGTTTCGTCGAGGATGCTGAAAGCTGTCGAAGGGCTAGSCCGCTGGT 160
NUMBER OF SEQ ID NOS: 137	Qy	1.277 GTGAGTGGTGGAGAGATGCTCACTTGGGCAAAGCTGGGACTACCGTGGCTCTT 1336
SOFTWARE: FastSEQ for Windows Version 4.0	Db	159 GTGAGTGGTGGAGAGATGCTCACTTGGGCAAAGCTGGGACTACCGTGGCTCTT 100
SEQ ID NO: 53	Qy	
TYPE: DNA	Db	
ORGANISM: Mycobacteria tuberculosis	Qy	1.337 TCCRGCGCGCGGAAGGTTGGATGGACGTAATGGATGCGCTGCGGCGGCC 1396
US-10-647-089-53	Db	99 TCCRGCGCGCGGAAGGTTGGATGGACGTAATGGATGCGCTGCGGCGGCC 40
Query Match 73.0%; Score 1119; DB 7; Length 1119;	Qy	
Best Local Similarity 100.0%; Pred. No. 1.3e-295; Mismatches 0; Indels 0; Gaps 0;	Db	
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1.397 TCGACCGTGTGGCTGAGGATGCTGGCTGGGAACTGGTACGGCAC 1435
317 CGTGCGCGCGAGGACTGGCCACTGGCTGGCTGGCTGGCTGG 376	Db	39 TCGACCGTGTGGCTGAGGATGCTGGCTGGCAAGCTGGTACGGCAC 1
1119 GCGTCGACAGCGCGGTGTCGAGGCGGACAGCGACATCCAGGCGG 1060	Qy	
377 CGTGCGCGCGAGGACTGGCCACTGGCTGGCTGGCTGGCTGG 436	Db	
1059 CGTGCGCGCGAGGACTGGCCACTGGCTGGCTGGCTGGCTGG 1000	Qy	
437 GTCCTGCGAGGATGGGATTCGGGGATGGGGATGGGGATGGGG 496	Db	
999 GTCCTGCGAGGATGGGATTCGGGGATGGGGATGGGGATGGGG 940	Qy	
497 GCGCCCTCGGCCTGAACTGGGATTCGGGGATGGGGATGGGG 556	Db	
939 GCGCCCTCGGCCTGAACTGGGATTCGGGGATGGGGATGGGG 880	Qy	
557 GATGAGTCCTCCGGGGCTCCGGGAAGGGATGGCTAACGTGGC 616	Db	
879 GATGAGTCCTCCGGGGCTCCGGGAAGGGATGGCTAACGTGGC 820	Qy	
617 CGCATGCCGACCCCTCGTCACCGAACCTGGGGTGTGCGCA 676	Db	
819 CGATGCCGACCCCTCGTCACCGAACCTGGGGTGTGCGCA 760	Qy	
677 CATGCCCTGGCTGGGGGATGGGAACCTGGGGTGTGCGCA 736	Db	
759 CATGCCCTGGCTGGGGGATGGGAACCTGGGGTGTGCGCA 700	Qy	
737 ATGCCCGCTGGGGGATGGGAACCTGGGGTGTGCGCA 796	Db	
699 ATGCCCGCTGGGGGATGGGAACCTGGGGTGTGCGCA 640	Qy	
797 GTCGATGGCTGAGGCACTGGGGATGGGAACCTGGGGTGTGCG 856	Db	
639 GTCGATGGCTGAGGCACTGGGGATGGGAACCTGGGGTGTGCG 580	Qy	
857 CAACGCAATCCATATCATCGGAGGATGGGAACCTGGGGTGTGCG 916	Db	
579 CAACGCAATCCATATCATCGGAGGATGGGAACCTGGGGTGTGCG 520	Qy	
917 ATGGCCGTCCTCCATATCATCGGAGGATGGGAACCTGGGGTGTGCG 460	Db	
519 ATGGCCGTCCTCCATATCATCGGAGGATGGGAACCTGGGGTGTGCG 308	Qy	
RESULT 6	Db	
US-10-647-089-53	Qy	US-10-282-122A-28776/c
		; Sequence 28776, Application US/1028212A
		; Publication No. US20040029129A1
		GENERAL INFORMATION:
		; APPLICANT: Wang, Liangsu
		; APPLICANT: Zamudio, Carlos
		; APPLICANT: Malone, Cheryl
		; APPLICANT: Haselbeck, Robert
		; APPLICANT: Ohlsen, Kari
		; APPLICANT: Zyskind, Judith
		; APPLICANT: Wall, Daniel
		; APPLICANT: Trawick, John
		; APPLICANT: Carr, Grant
		; APPLICANT: Yamamoto, Robert
		; APPLICANT: Forsyth, R.
		Xu, H.
		TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
		FILE REFERENCE: ELTRA-034A
		CURRENT APPLICATION NUMBER: US/10/282,122A
		CURRENT FILING DATE: 2003-02-20
		PRIOR APPLICATION NUMBER: 60/191,078
		PRIOR FILING DATE: 2000-03-21
		PRIOR APPLICATION NUMBER: 60/206,848
		PRIOR FILING DATE: 2000-05-23
		PRIOR APPLICATION NUMBER: 60/207,727
		PRIOR FILING DATE: 2000-05-26
		PRIOR APPLICATION NUMBER: 60/230,335
		PRIOR FILING DATE: 2000-09-06
		PRIOR APPLICATION NUMBER: 60/230,347
		PRIOR FILING DATE: 2000-09-09
		PRIOR APPLICATION NUMBER: 60/242,578
		PRIOR FILING DATE: 2000-10-23
		PRIOR APPLICATION NUMBER: 60/253,625
		PRIOR FILING DATE: 2000-11-27
		PRIOR APPLICATION NUMBER: 60/257,931
		PRIOR FILING DATE: 2000-12-22
		PRIOR APPLICATION NUMBER: 60/267,636
		PRIOR FILING DATE: 2001-02-09
		PRIOR APPLICATION NUMBER: 60/269,308
		ATGGCCGTCCTCCATATCATCGGAGGATGGGAACCTGGGGTGTGCG

RESULT 7
US-10-282-122A-25931/c
; Sequence 25931; Application US/10282122A
; Publication No. US2004009129A1
GENERAL INFORMATION:
; APPLICANT: Wang, Liangshu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cherry L
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlseni, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Hall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsby, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25931
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25931

Query Match 27.1%; Score 415.2; DB 7; Length 1023;
Best Local Similarity 68.0%; Pred. No. 2, 7e-103;
Matches 651; Conservative 0; Mismatches 253; Indels 54; Gaps 4
Qy 390 AGCTTGCGGCCATGGTCTGGGATGGCGCGATGGTTCTGGAGCGGCCCTGC- -GCCCGCGGTGCTGCAGC
Db 959 AGCTTGCGGCCGAACCGTTCACTGGTCCAGGCTTGCAGGCTTGGTGCAGGGTGCAGC 9
Qy 447 GCAGCAATGGCGTTCGGGATGGCGCGATGGTTCTGGAGCGGCCCTGC
Db 899 GCAGCGGGGATTCGGGGTACTGGGGTCTGGGAAAGGATCAGTGGCATGCGCATGC 5
Qy 507 GGCGCTGAAAGC -- TTGGGATCTGGGAAAGGATCAGTGGCATGCGCATGCAGC 5
Db 839 GGTTGGGACCTGCTGGATGGCCAGAACGGATGGCTGGATGGCTGGGATGGCTGG 7
Qy 564 TCCCTGGCGCGGGCTCCGGGAAACGGTCCAGATGGTCAAACCTGGCGCATGC 6
Db 779 GATTGGTGAACGGTCCGGAGCTGGATGGCTGGATGGCTGGCATGGTCAATGCGCATGC 7
Qy 624 CCGGGACCTGGCTCAACAGAACCTGGGTCCACACCTGGTGTGGCACATGCT 6

RESULT 10
 US-10-647-089-52/c
 ; Sequence 52, Application US/10647089
 ; Publication No. US20040063923A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behr, Marcel
 ; APPLICANT: Small, Peter
 ; APPLICANT: Schoonnik, Gary
 ; APPLICANT: Wilson, Michael A.
 ; TITLE OF INVENTION: Molecular Differences Between Species of
 ; TITLE OF INVENTION: the M. Tuberculosis Complex
 ; CURRENT APPLICATION NUMBER: US/10/647,089
 ; CURRENT FILING DATE: 2003-08-21
 ; PRIORITY NUMBER: US/09/894,844
 ; FILE REFERENCE: STAN102CON
 ; PRIORITY NUMBER: 09/318,191
 ; PRIORITY FILING DATE: 1999-05-25
 ; PRIORITY APPLICATION NUMBER: 60/097,936
 ; PRIORITY FILING DATE: 1998-08-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 52
 ; LENGTH: 894
 ; TYPE: DNA
 ; ORGANISM: Mycobacteria tuberculosis
 US-10-647-089-52

Query Match 20.3%; Score 311; DB 7; Length 894;
 Best Local Similarity 100%; Pred. No. 8e-75; Mismatches 0; Indels 0; Gaps 0;

Query	Subject
Qy	1 ATGTTCAAGCTCGGAACCTCGATCCGGACCTGAAATCCATGCGGAAACCCGACCCGACC 60
Db	311 ATGTTCAAGCTCGGAACCTCGATCCGGACCTGAAATCCATGCGGAAACCCGACCCGACC 252
Qy	61 GCGTACCCGCCATTCAAACCGCGAACATCGATCCGGACCTGAAATCCATGCGGAAACCCGACCCGACC 120
Db	251 GCGTACCCGCCATTCAAACCGCGAACATCGATCCGGACCTGAAATCCATGCGGAAACCCGACCCGACC 192
Qy	121 AAGACGTTTCGAAGAACCGCGGAGATGAAACCGAGGATCTTGCTTAACGTGGCC 180
Db	191 AAGACGTTTCGAAGAACCGCGGAGATGAAACCGAGGATCTTGCTTAACGTGGCC 132
Qy	181 GAGGACTCGGATATCGTAAGGTCCGTGTCGAGCGAACGTTGGGGCGGTGAATGT 240
Db	131 GAGGACTCGGATATCGTAAGGTCCGTGTCGAGCGAACGTTGGGGCGGTGAATGT 72
Qy	241 ACCGGCCGGCCGAATGTTCTGCCCCATCACTTGGTAGGCCCTCGCTGTCGAGCGCTCTCGGG 300
Db	71 ACCGGCCGGCCGAATGTTCTGCCCCATCACTTGGTAGGCCCTCGCTGTCGAGCGCTCTCGGG 12
Qy	301 TTTGTCGACAT 311
Db	11 TTTGTCGACAT 1

Db	54	GCCGTCACGTCGGTACGGCATATCTTGTGGCGGACATAGGCTGTTGCTGGCTGGTCAACGTTGACACCA 1
		RESULT 12
		US-10-282-122A-25902/C
		Sequence 25902, Application US/10282122A
		Publication No. US20040029129A1
		GENERAL INFORMATION:
		APPLICANT: Wang, Liangsu
		APPLICANT: Malone, Carlos
		APPLICANT: Haselbeck, Robert
		APPLICANT: Malone, Cherry
		APPLICANT: Ohlsen, Kari
		APPLICANT: Zyskind, Judith
		APPLICANT: Wall, Daniel
		APPLICANT: Trawick, John
		APPLICANT: Carr, Grant
		APPLICANT: Yamamoto, Robert
		APPLICANT: Forsyth, R.
		APPLICANT: Xu, H.
		TITLE OF INVENTION: Identification of Essential Genes in Microorganism
		FILE REFERENCE: ELTRA.034A
		CURRENT APPLICATION NUMBER: US/10/282,122A
		CURRENT FILING DATE: 2003-02-10
		PRIOR APPLICATION NUMBER: 60/191,078
		PRIOR FILING DATE: 2000-03-21
		PRIOR APPLICATION NUMBER: 60/206,848
		PRIOR FILING DATE: 2000-05-23
		PRIOR APPLICATION NUMBER: 60/207,727
		PRIOR FILING DATE: 2000-05-26
		PRIOR APPLICATION NUMBER: 60/230,335
		PRIOR FILING DATE: 2000-09-06
		PRIOR APPLICATION NUMBER: 60/230,347
		PRIOR FILING DATE: 2000-09-09
		PRIOR APPLICATION NUMBER: 60/242,578
		PRIOR FILING DATE: 2000-10-23
		PRIOR APPLICATION NUMBER: 60/253,625
		PRIOR FILING DATE: 2000-11-27
		PRIOR APPLICATION NUMBER: 60/257,931
		PRIOR FILING DATE: 2000-12-22
		PRIOR APPLICATION NUMBER: 60/257,636
		PRIOR FILING DATE: 2001-02-09
		PRIOR APPLICATION NUMBER: 60/269,308
		PRIOR FILING DATE: 2001-02-16
		Remaining Prior Application data removed - See File Wrapper or PALM
		NUMBER OF SEQ ID NOS: 78614
		SOFTWARE: PatentIn version 3.1
		SEQ ID NO: 25902
		LENGTH: 276
		TYPE: DNA
		ORGANISM: Mycobacterium avium
		US-10-282-122A-25902
		Query Match 6.8%; Score 104.8; DB 7; Length 276;
		Best Local Similarity 75.6%; Pred. No. 1.7e-18;
		Matches 130; Conservative 0; Mismatches 42; Indels 0; Gap 0
Qy	1122	GCGCGGAACACGTCGGTACCGCTGCGCTACTCAGGGATGATCCACGGAACTGGTTCTGTGGCTGGCG
Db	173	GGCGGAAGGGTTGGATGCCGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
Qy	1182	GTGCACGCGCTGCTGGCGACGATGATCTCCACGGAACTGGTTCTGTGGCTGGCTGGCTGGCTGGCTGG
Db	113	GTGAGGGATCGTGGCGACGATGCCGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
Qy	1242	CTGTCGAAGGCTGAGGGGTAGCCCGCCCTGGTTGAGTGGTCCAGACGA 1294
Db	53	CCGTCACAGTGTGGCGACATAGGCTGTTGGTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG

```

Sequence 13587, Application US/10282122A1
Publication No. US201004029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangshu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Yu, H.

TITLE OF INVENTION: Identification of Burkholderia fungorum
FILE REFERENCE: ELTRIA 03A
CURRENT APPLICATION NUMBER: US/10/282,117
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO: 13587
LENGTH: 951
TYPE: DNA
ORGANISM: Burkholderia fungorum
us-10-282-122A-13587

Query Match 4.7%; Score 72
Best Local Similarity 54.5%; Pred. No
Matches 146; Conservative 0; Mismatches
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Db 275 TCGTCGGCTCGATGTTGGATGAATT
Qy 1086 TTCCCATTTGGGCCAGGTTCGCTTC
Db 215 TTGCGTGCAGCCSACGTTGGTGNCGTGT
Qy 1146 TCGGCCTAACGATGATGTCGGTGCAGACCA
Db 155 GCGCCGAAAGGAACTCAGTACAGCCAGTGTG
Qy 1206 ATCTCCACCGGAAGTCGTTTGCTGGTC
Db 95 ATCTCGAAATGGCACATGAGATGCTGGTGT
Qy 1266 CCGCCTGGTGTGTCGGTGCAGACCA
Db 35 TCGCTCGCCGTTAACAAAGCACCAGTGA

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RESULT 14
 US-282-122A-35893/C
 / Sequence 35893, Application US/10282122A
 / Publication No. US20040029129A1
 / GENERAL INFORMATION:
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Forsyth, R.
 / APPLICANT: Xu, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELTRA-034A
 / CURRENT APPLICATION NUMBER: US/10/282,122A
 / CURRENT FILING DATE: 2003-02-20
 / PRIOR APPLICATION NUMBER: 60/191,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: 60/230,335
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/257,931
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 78614
 / SOFTWARE: PatentIn version 3.1
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 / TYPE: DNA
 / ORGANISM: Streptococcus mutans
 US-10-282-122A-35893

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 Db 332 TCTTAAGATCAATTGTTTGAAGTTAAAGGGTCTTCATAATCATCATTCA 273
 Qy 1038 CACAACGGGACCTACTGCCGGAGACACCTGGGGTACCGCTCGGCCTACTCA 1157
 Db 272 CATCTGGATGATGACTGTCTAGCTTCTAACAAATTCGACCAAAGTTTGTAATT 213
 Qy 1098 CGGAGTTTCGTTCTGAGATCGGGGGTGGATGGTCACTGGTGGCGACGATGATCTCCACCGG 1217
 Db 212 CCTTGATTTCTGATTAAGAAAGCCGAATTAAATCTGATACTGTTGATAGGT 153
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 Qy 1218 AAGTCGGTTCTGGTCAAGAGAGCTCGAGGGCTGAGGGCTGAGCCGCTGGT 1277
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Qy 1278 TGAGTGGTCAAGAGATGCTGCTCACCT 1303
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RESULT 15
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 / Sequence 1, Application US/09976059
 / Patent No. US20020164747A1
 / GENERAL INFORMATION:
 / APPLICANT: Farnec, Chris
 / APPLICANT: Zopoulos, Emmanuel
 / APPLICANT: Staffa, Alfredo
 / TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
 / FILE REFERENCE: 3019-PCT
 / CURRENT APPLICATION NUMBER: US/09/976,059
 / CURRENT FILING DATE: 2001-10-15
 / NUMBER OF SEQ ID NOS: 34
 / SOFTWARE: PatentIn version 3.0
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 / ORGANISM: Actinoplanes sp.
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 / OTHER INFORMATION: ORF 6; negative strandedness
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 / OTHER INFORMATION: ORF 9; negative strandedness
 / NAME/KEY: misc feature
 / LOCATION: (15203)..(13614)
 / OTHER INFORMATION: ORF 10; negative strandedness
 / NAME/KEY: misc feature
 / LOCATION: (19032)..(39713)
 / OTHER INFORMATION: ORF 11; positive strandedness
 / NAME/KEY: misc feature
 / LOCATION: (39713)..(65800)
 / OTHER INFORMATION: ORF 14; positive strandedness
 / NAME/KEY: misc feature
 / LOCATION: (65826)..(66530)
 / OTHER INFORMATION: ORF 15; positive strandedness

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 OTHER INFORMATION: ORF 23; positive strandedness

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 OTHER INFORMATION: ORF 24; negative strandedness

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 OTHER INFORMATION: ORF 27; negative strandedness

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 OTHER INFORMATION: ORF 30; positive strandedness

NAME/KEY: misc_feature
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 OTHER INFORMATION: ORF 31; positive strandedness

NAME/KEY: misc_feature
 LOCATION: (87372) .. (86803)
 OTHER INFORMATION: ORF 32; positive strandedness

NAME/KEY: misc_feature
 LOCATION: (87494) .. (88420)
 OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only

US-09-976-059-1

Query Match 3.7%; Score 57.4; DB 3; Length 88421;
 Best Local Similarity 43.4%; Pred. No. 2.1e-05;
 Matches 262; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

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Qy	733	CGCCATGACAGCGCTGGACATACAGTCAAGGCCATAGCTGGTGGGGAA	792
Db	40760	CCACCTGGAACAGCGGGTGGGCTCAGCGCCGAACTGGCCGAGCTCTGGGCTCAGCGACT	40701
Qy	793	TGTGTCCTAGCGCTGGCGACGCTGAGCTGGTGGCTGAGCTGGTGGCTGAGCTGGGAA	852
Db	40700	TCTGAAGCGAAGTGTGCTGGCTAGCGTGGCCGAGCTGGCTCAGCTGGCGCA	40641
Qy	853	AGATCAAAGCATCAGGCTCAAGTTGCCCGAACCGGGGGAAACTCGAGTCCT	912

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OM nucleic - nucleic search, using SW model

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 (without alignments)

6500.886 Million cell updates/sec

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 Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

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 4: /cgm2_6/ptodata/1/pubna/PCT_NEW_PUB.seq;*
 5: /cgm2_6/ptodata/1/pubna/US09_NEW_PUB.seq;*
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 7: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq;*
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 9: /cgm2_6/ptodata/1/pubna/US13_NEW_PUB.seq;*
 10: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq2;*
 11: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq3;*
 12: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq4;*
 13: /cgm2_6/ptodata/1/pubna/US60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1533	100.0	12732	8 US-10-802-796-1 Sequence 1, Appli
c 2	1119	73.0	1119	12 US-11-143-401-53 Sequence 53, Appli
c 3	31.1	20.3	894	12 US-11-143-401-52 Sequence 52, Appli
c 4	57.4	3.7	88421	12 US-11-005-109-1 Sequence 1, Appli
c 5	55.6	3.7	1236	12 US-11-143-401-127 Sequence 127, Appli
c 6	53	3.5	2155	12 US-11-122-329-122 Sequence 122, Appli
c 7	53	3.5	2937	9 US-11-202-566-8 Sequence 8, Appli
c 8	53	3.5	6200	8 US-10-895-011-1 Sequence 1, Appli
c 9	53	3.5	6200	12 US-11-038-372-1 Sequence 1, Appli
c 10	53	3.5	3700	8 US-10-522-037-1 Sequence 133, Appli
c 11	49.6	3.2	1386	8 US-10-898-730-133 Sequence 35, Appli
c 12	47.2	3.1	10368	12 US-11-075-185-35 Sequence 1, Appli
c 13	47.2	3.1	78869	12 US-11-075-185-1 Sequence 78, Appli
c 14	45.4	3.0	1356	12 US-11-024-959-78 Sequence 36, Appli
c 15	45.5	2.9	5679	12 US-11-075-185-36 Sequence 3, Appli
c 16	44.8	2.9	897	8 US-10-432-483-3 Sequence 6, Appli
c 17	44.8	2.9	3624	7 US-10-432-483-48 Sequence 48, Appli
c 18	44.8	2.9	8551	8 US-10-432-483-48 Sequence 40, Appli
c 19	44.6	2.9	5301	12 US-11-075-185-40 Sequence 762706,
c 20	43.8	2.9	607	6 US-09-925-065A-830710 Sequence 830710, Appli

ALIGNMENTS

RESULT 1
 US-10-802-796-1
 / Sequence 1, Application US/10802796
 / Publication No. US20050250104A1
 / GENERAL INFORMATION:
 / APPLICANT: COLE, STEWART
 / APPLICANT: BUCHHEISER-BROSCH, ROLAND
 / APPLICANT: BILLAULT, ALAIN
 / APPLICANT: GORDON, STEPHEN
 / TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.
 / FILE REFERENCE: 05394 .0011-00000
 / CURRENT APPLICATION NUMBER: US-10-802-796
 / CURRENT FILING DATE: 2004-03-18
 / PRIOR APPLICATION NUMBER: US/09/673,476
 / PRIOR FILING DATE: 2002-03-29
 / PRIOR APPLICATION NUMBER: PCT/IB99/00740
 / PRIOR FILING DATE: 1999-04-16
 / PRIOR APPLICATION NUMBER: 09/060,756
 / PRIOR FILING DATE: 1998-04-16
 / SOFTWARE: PatentIn Ver. 2.2
 / SEQ ID NO 1
 / LENGTH: 12732
 / TYPE: DNA
 / ORGANISM: Mycobacterium tuberculosis
 / Query Match 100.0%; Score 1533; DB 8; Length 12732;
 / Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GATGAGCTCCTCGGGCGGGGTCTCCCGGAACAGGTGAGGATCGGGTCAAAACGTTGC 616 ; CURRENT APPLICATION NUMBER: US/11/143,401
 Db 879 GATGAGCTCCTCGGGCGGGGTCTCCCGGAACAGGTGAGGATCGGGTCAAAACGTTGC 820 ; PRIOR APPLICATION DATE: 2005-06-01
 QY 617 CGCATGCCCGAACCTGGTCAACAGAACCTTGCGGGTCCACCGTGGTGTGCA 676 ; PRIOR APPLICATION NUMBER: US/10/647,089
 Db 819 CGATGCCCGAACCTGGTCAACAGAACCTTGCGGGTCCACCGTGGTGTGCA 760 ; PRIOR FILING DATE: 2003-08-21
 Db 677 CAGCCCTTGGTGGTGGGATAACGCCCATGGGAAACATGGGATGTCCC 736 ; PRIOR APPLICATION NUMBER: US/09/894,844
 QY 759 CAGCCCTTGGTGGTGGGATAACGCCCATGGGAAACATGGGATGTCCC 700 ; PRIOR FILING DATE: 2001-06-27
 Db 737 ATGACCGGGTGGGACTGGAGATACAGTCAGGCAATGGGAGAATSTC 796 ; PRIOR APPLICATION NUMBER: 09/318,191
 QY 699 ATGACCGGGTGGGACTGGAGATACAGTCAGGCAATGGGAGAATSTC 640 ; PRIOR FILING DATE: 1999-05-25
 Db 699 ATGACCGGGTGGGACTGGAGATACAGTCAGGCAATGGGAGAATSTC 640 ; SOFTWARE: FastSEQ For Windows Version 4.0
 QY 797 GTCTAGGCCCTGGGACGGTACAGCCGAGTTGGATGAGGTTCATCAAGT 856 ; SEQ ID: NO 52
 Db 639 GTCTAGGCCCTGGGACGGTACAGCCGAGTTGGATGAGGTTCATCAAGT 580 ; TYPE: DNA
 QY 857 CAAGCATCAGGTCAAGTTGCCCGAACCGGGGAACTCGAGTCCTTGC 916 ; ORGANISM: Mycobacteria tuberculosis
 Db 579 CAAGCATCAGGTCAAGTTGCCCGAACCGGGGAACTCGAGTCCTTGC 520 ; US-11-143-401-52
 QY 917 ATGCCCGTCTCCATATACTCGACCGGATGCAAGCAACCGGGGAACTCGAGTCCTTGC 976 ; Query Match Score: 311; Best Local Similarity: 100.0%; Matches: 311; Conservative: 0; Indels: 0; Gaps: 0;
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 QY 977 GTCGAGGAATGGCACCTGTTGCTTAGTTCAAGGTGATGATCAGTAGTCAGTTCCGCTC 1036 ; Number of SEQ ID NOS: 137
 Db 459 GTCGAGGAATGGCACCTGTTGCTTAGTTCAAGGTGATGATCAGTAGTCAGTTCCGCTC 400 ; SOFTWARE: FastSEQ For Windows Version 4.0
 QY 1037 GCACAAACGGGACCTACTCCCGGAGACCTGGGATGCAAGTCCATTGAG 1096 ; NUMBER OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
 Db 399 GCACAAACGGGACCTACTCCCGGAGACCTGGGATGCAAGTCCATTGAG 340 ; FILE REFERENCE: 3002-2US
 QY 1097 GCGGAGGTTTCGCTCCNGAAGATGCGGGACACCTGGGATGCAAGTCCATTGAG 1156 ; CURRENT APPLICATION NUMBER: US/11/205,109
 Db 339 GCGGAGGTTTCGCTCCNGAAGATGCGGGACACCTGGGATGCAAGTCCATTGAG 280 ; PUBLICATION NUMBER: US20050287641A1
 QY 1157 ACCGATGATGCCGGGGTGGCATGGTGGCATGGTGGGCAACGATCTCCACCGG 1216 ; SEQUENCE 1, Application US/11143401
 Db 279 ACCGATGATGCCGGGGTGGCATGGTGGCATGGTGGGCAACGATCTCCACCGG 220 ; PRIORITY NUMBER: US/09/976,059
 QY 1217 GAAGTCGGTTGGTGGTGGAGAAGCTTGAGGGCTGAGGGCTGAGCCCTGGT 1276 ; PRIORITY FILING DATE: 2001-10-15
 Db 219 GAAGTCGGTTGGTGGTGGAGAAGCTTGAGGGCTGAGGGCTGAGCCCTGGT 160 ; PRIORITY APPLICATION NUMBER: US/09/976,059
 QY 1277 GTGAGTGGTGGAGAAGCTGGTGGCATGGTGGGAAAGCTGGGACTCAACCGTGGCCCTT 1336 ; PRIORITY APPLICATION NUMBER: US/09/976,059
 Db 159 GTGAGTGGTGGAGAAGCTGGTGGCATGGTGGGAAAGCTGGGACTCAACCGTGGCCCTT 100 ; PRIORITY APPLICATION NUMBER: US/09/976,059
 QY 1337 TCCTCGGGGCCAGGGTATGGGATGGGAAAGCTGGGACTCAACCGTGGCCCTT 1396 ; PRIORITY APPLICATION NUMBER: US/09/976,059
 Db 99 TCCTCGGGGCCAGGGTATGGGATGGGAAAGCTGGGACTCAACCGTGGCCCTT 40 ; PRIORITY FILING DATE: 2000-10-15
 QY 1397 TCGACCGTGTGGCTGGTGGGCAAGCTGGTGGGAAAGCTGGGACTCAACCGTGGCCCTT 1435 ; PRIORITY APPLICATION NUMBER: US/09/976,059
 Db 39 TCGACCGTGTGGCTGGTGGGAAAGCTGGTGGGAAAGCTGGGACTCAACCGTGGCCCTT 1 ; PRIORITY FILING DATE: 2000-10-15
 RESULT 3 US-11-143-401-52/c ; Sequence 52, Application US/11143401
 ; GENERAL INFORMATION: ; Publication No. US2006002953A1
 ; APPLICANT: Behr, Marcel ; SEQ ID NO 1
 ; APPLICANT: Schoolnik, Gary ; LENGTH: 88421
 ; APPLICANT: Wilson, Michael A. ; PEASURE: misc feature
 ; TITLE OF INVENTION: Molecular Differences Between Species of ; NAME/KEY: misc feature
 ; TITLE OF INVENTION: the M. Tuberculosis Complex ; LOCATION: (2077) .. (3078)
 ; FILE REFERENCE: STAN102CON ; OTHER INFORMATION: ORF 1, positive strandedness

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NAME/KEY: misc feature
LOCATION: (7703)..(6632) OTHER INFORMATION: ORF 5; negative strandedness
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LOCATION: (812346)..(82062) OTHER INFORMATION: ORF 28; negative strandedness
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NAME/KEY: misc feature
LOCATION: (867372)..(86803) OTHER INFORMATION: ORF 32; negative strandedness
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LOCATION: (874941)..(88420) OTHER INFORMATION: ORF 33; positive strandedness
US-11-205-109-1

Query Match Score 3.7;
Best Local Similarity 43.4%; Pred. No. 2.6e-05;
Matches 262; Conservative 341; Indels 0; Gaps 0;

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Db 40820 GCGAGGGGACCCGGGACTGGCTCAAGTCGGCTCAGTCGGAGGG 40761
Qy 733 CGCCATGCCCGGTGGAGCTGAGATCAGTCAGCTGGCAGGAA 792
Db 40760 CCACCTGAACAGGGCTGGGGCTGGCTGGCTGGCTGGAGCTGGAGCT 40701
Qy 793 TCTCTGCTGAGCTGGCTGAGGCTAACGGCCAGTTGCTGATGAGTCATCA 852
Db 40700 TCTCTGAAACGGCACGTCTGGCTGGCTGGCTGGAGCTGGCCCA 40641

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Db	40640	GCAGGTCCGGAAAGGTCGGTCCGGTCAAGGTGGCCGATCACGGTTGTTGAGA	40581	Qy	1468	GTGGGCTCGAACCGC	1483
Qy	913	TGGCATGGCGTCTCCATATCACTCCGACGGATAAGAACCGTCGCTTGGGT	972	Db	942	GTGTCCTGGAAACGC	927
Db	40580	AGCAGCCGACGAGGCGTGTGAGGCCGCCCCGTCGACCGTCGATCG	40521				
Qy	973	GCCGGTCAAGGATGCGACCTGGCTAGCTTCAGGGATGATCAAGTAGTCGTCG	1032		RESULT 6		
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Qy	1033	CCTGGCACACGGACGTAATCCCGGAGGCGCTCAAGGGCTTCAGTTCCAT	1092		; Sequence 122, Application US/11-122329		
Db	40460	TGAAGGGGGTGGCGGCGAGTCGGGTTAGTCGCGCTGGGGCGCG	40401		; Publication No. US20060019272A1		
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Db	40400	GCAGGCCGAACTGGCGTGTGGCCCGGCAACGACGAGCGCCGGCG	40341		; APPLICANT: Geraci, Mark		
Qy	1153	ACTACGGATGATGCCGGGTGCAATGGTCGAGCTCGTGGCGAGAT	1212		; APPLICANT: Bull, Todd		
Db	40340	CCGGCAGGGCACTTCGGGGCTCCGGGACGGCAAATAGCGGACCTGT	40281		; APPLICANT: Voelkel, Norbert		
Qy	1213	CCGGAAAGTCGGTTGCTGCTGAGAAGCTGTCGAGGCTGAGCCCCT	1272		; APPLICANT: Coldren, Chris B		
Db	40280	CGGGCAGGGGCTTCGGGTCTCAGGCGACCTCTGTGTCGACAGGGGT	40221		; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Genes		
Qy	1273	GGT	1275		; TITLE OF INVENTION: Expression Analysis of Peripheral Blood Cells		
Db	40220	AGT	40218		; FILE REFERENCE: 2848-54		
Qy	11-143-401-127/c	Sequence 127, Application US/11143401			; CURRENT APPLICATION NUMBER: US/11-122,329		
		Publication No. US20060002953A1			; CURRENT FILING DATE: 2005-05-03		
		APPLICANT: Behr, Marcel			; PRIOR APPLICATION NUMBER: 60/568,129		
		APPLICANT: Small, Peter			; PRIOR FILING DATE: 2004-05-03		
		APPLICANT: Schoolnik, Gary			; NUMBER OF SEQ ID NOS: 128		
		APPLICANT: Wilson, Michael A.			; SOFTWARE: Patentin version 3.3		
		TITLE OF INVENTION: Molecular Differences Between Species of			; SEQ ID NO: 122		
		FILE REFERENCE: SPAN102CON			; LENGTH: 2155		
		CURRENT APPLICATION NUMBER: US/11/143,401			; TYPE: DNA		
		CURRENT FILING DATE: 2005-06-01			; ORGANISM: Homo sapiens		
		PRIOR APPLICATION NUMBER: US/10/547,089			; LENGTH: 1222		
		PRIOR FILING DATE: 2003-08-21					
		PRIOR APPLICATION NUMBER: US/09/894,844					
		PRIOR FILING DATE: 2001-06-27					
		PRIOR APPLICATION NUMBER: 09/318,191					
		PRIOR FILING DATE: 1999-05-25					
		PRIOR APPLICATION NUMBER: 60/097,936					
		PRIOR FILING DATE: 1998-08-25					
		NUMBER OF SEQ ID NOS: 137					
		SOFTWARE: FastSEQ for Windows Version 4.0					
		SEQ ID NO: 127					
		LENGTH: 1236					
		TYPE: DNA					
		ORGANISM: Mycobacteria tuberculosis					
		US-11-143-401-127					
Qy	1348	CGCAAGGGTATTGGGATGGAAAGCTGAGATCCCTGCGCCGCGTCTG	1407	Qy	1348	CGCAAGGGTATTGGGATGGAAAGCTGAGATCCCTGCGCCGCGTCTG	1407
Db	1062	CGTGGGGTGTAGTAGTGCGCCCTCATGGTGTACAGGAAACGC	1003	Db	1062	CGTGGGGTGTAGTAGTGCGCCCTCATGGTGTACAGGAAACGC	1003
Qy	1408	GGCTCTGGGTCCGGGAGATAGGGCAAGCTTGGGTCACCAACCTGTG	1467	Db	1228	CTGCTCTCATCGAGCGCAGAGCCCCATGGGTGAGCACGACAG	1221
		GTGACATGGGTCACAGGAAACTTGGGTCACCAACCTGTG	695	Qy	677	CTGCTCTGGGGTGGGG	695
		GTGACATGGGTCACAGGAAACTTGGGTCACCAACCTGTG	1210	Db	1228	CTGCACTGGGGGGGG	1210

CURRENT APPLICATION NUMBER: US/11/202,566
 PRIORITY FILING DATE: 2005-08-12
 PRIORITY APPLICATION NUMBER: US/10/600,862
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 8
 LENGTH: 2937
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: RAP-IDU fusion sequence
 US-11-202-566-8

Query Match 3.5%; Score 53; DB 8; Length 6200;
 Best Local Similarity 48.0%; Pred. No. 0.00032;
 Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
 Qy 319 CTCGACAGCCGGTCCAGGGAAACATCCACAGGCCACTCCCGTGGGTGCA 377
 Db 3051 CTGCTCTGGCTGGGAGGGGAAAGGGCCAGGGCACTCCCGTGGGTGCA 2992
 Qy 378 -GTCGGCGGGGAGGGGAAAGGGGAAAGGGCCAGGGCACTCCCGTGGGTGCA 436
 Db 2991 GAGCCCTTGTCCAGTAGCGCTGGGTAGAACAGCAGGGGACCCGGG 2932

Query Match 3.5%; Score 53; DB 9; Length 2937;
 Best Local Similarity 48.0%; Pred. No. 0.00031;
 Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
 Qy 319 CTCGACAGCCGGTCCAGGGCACACATCCAGGCCCTGGGCTGGC- 377
 Db 2469 CTGCTCTGGCTGGGAGGGGAAAGGGCCAGGGCACTCCCGTGGGTGCA 2410
 Qy 378 -GTCGGGGGGAGGGTGGGCACTGGGTCTTGAGCGGGGGGGGGGGGGG 436
 Db 2409 GAGCCCTTGTCCAGGTAGCGCTGGGTAGCTAGAACAGGGGACCCGGG 2350
 Qy 437 CTGCTGAGCCGGCAGATGGGCACTGGGTCTTGAGGGGGGGGGGGGG 496
 Db 2349 CAGCCGAGGGTCACTGGGCACTGGGTGGGTGGGTGGGTGGGTGCA 2290
 Qy 497 GGCCTCTCGGGGCGCTGAACCTGGGATCTGGGAACTGGGCAATGAGGC 556
 Db 2289 GATCAGAACGGCGGGCGCCAGGGCTGGGGCTGGGGCTGGCAG 2230
 Qy 557 GATGAGCTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 616
 Db 2229 GAGGCCAACGGTGGGTGCTGGGCACTGGGGCTGGGGCTGGGG 2170

RESULT 9
 US-11-038-372-1/c
 Sequence 1, Application US/11038372
 Publication No. US2005260195A1
 GENERAL INFORMATION:
 APPLICANT: KAKKIS, EMIL D.
 TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
 FILE REFERENCE: 008000051CNUS01
 CURRENT APPLICATION NUMBER: US/11/038,372
 PRIOR APPLICATION NUMBER: 008000051CNUS01
 CURRENT FILING DATE: 2005-01-18
 PRIOR FILING DATE: 2004-07-20
 PRIOR APPLICATION NUMBER: US/10/895,011
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: 09/711,205
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 09/439,923
 PRIOR FILING DATE: 1999-11-12
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 1

LENGTH: 6200
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1558) . . . (3510)

Query Match 3.5%; Score 53; DB 12; Length 6200;
 Best Local Similarity 48.0%; Pred. No. 0.00032;
 Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
 Qy 319 CTCGACAGCCGGTCCAGGGAAAGGGCCACATCCAGGGCCACTCCCGTGGGTGCA 377
 Db 3051 CTGCTCTGGCTGGGAGGGGAAAGGGCCAGGGCACTCCCGTGGGTGCA 2992


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RESULT 13
US-11-075-185-1/c
; Sequence 1, Application US/11075185
; Publication No. US20050266424A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULLEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 011059.03
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

Query Match    3.1%; Score 47.2; DB 12; Length 78869;
Best Local Similarity 45.8%; Pred. No. 0..011; Indels 0; Gaps 0;
Matches 163; Conservative 0; Mismatches 193;

Qy          335 GAGCCGGAGGGCACACATCCAGGACCCCCCTCGGCCTCGGCCGGGAGGCTT 394
Db          24306 GCGCTCGCTCGGCCGGCAAGCGCCACCCGCTCCGTGGTGTGCCGGCTGGAA 24247
Qy          395 GCGCCACTGGCTCTTGACCCGGCGCCGGGTGCGCCCGGCTGGTGTGCCGGCAGCAT 454
Db          24246 CGCCCCAACGGCGAACCGGCCCTCGTGTTCAGGGGAGCTGGATGACGGTGTGAG 24187
Qy          455 GGCGATCGGGGGATGGCGCATGGTTTCCCTGCAGGGCGGCCCTCCGGCTCTGG 514
Db          24186 CCCCTCCCGCTCGTGTCCGGCTGTGGTGTTCAGGGGAGCTGGATGACGGTGTGAG 24127
Qy          515 AACGTTGGCATCTGGAAAGATCCGGCCATGAGCTCCGGCATGAGCTCCGGCSC 574
Db          24126 CGCCCTGATCAGACCTCCGAAACCGGAACCCAGAACCTGGTCTGGACGCC 24067
Qy          575 GGGGTTCCGGAAAGGGTGGCATGGTCAAGCTGGGATGCGGATGCCAGACCTCTGG 634
Db          24066 CTCCCTCTGGCGAACGGCGCAAGACTGGGATGCGGATGCCAGACCTCTGG 24007
Qy          635 CGTCAACAGAACATTGGCGGGTCCACACTGGCTGGCATGGCTGGGAT 690
Db          24006 GATCCGGAAAGCTGGTCCGGCACCGGTGGCAGCGAACCGGCTGGAT 23951

RESULT 14
US-11-024-959-78/c
; Sequence 78, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-036 CY
; CURRENT FILING DATE: 2004-12-30
; CURRENT APPLICATION NUMBER: US/11/024, 959
; PRIOR APPLICATION NUMBER: 60/533,036

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26	34.8	2.5	66628	3	US-09-049-16-16112	Sequence 16112, A
27	34.8	2.4	888	3	US-09-049-002-540-8531	Sequence 8531, Ap
28	34.4	2.4	1410	3	US-09-002-540-4936	Sequence 4936, Ap
29	34.4	2.4	8518	3	US-09-092-540-8894	Sequence 8894, App
30	34.4	2.4	30780	3	US-09-002-540-1243	Sequence 1243, A
31	34.2	2.4	1040	3	US-09-072-596-307	Sequence 307, App
32	34.2	2.4	1040	3	US-09-072-967-310	Sequence 310, App
33	34.2	2.4	1040	3	US-10-193-000-307	Sequence 307, Ap
34	34.2	2.4	1040	3	US-10-084-843-312	Sequence 312, App
35	33.8	2.4	738	3	US-09-052-991A-1829	Sequence 1289, A
36	33.8	2.4	1083	3	US-09-252-991A-13113	Sequence 13113, A
37	33.8	2.4	1254	3	US-09-052-991A-12950	Sequence 12950, A
38	33.8	2.4	1272	3	US-09-052-991A-125230	Sequence 12523, A
39	33.8	2.4	1431	3	US-09-252-991A-8674	Sequence 8674, Ap
40	33.8	2.4	1767	3	US-09-052-991A-8570	Sequence 8570, Ap
41	33.8	2.4	19455	3	US-09-002-540-1147	Sequence 1147, Ap
42	33.8	2.4	263693	3	US-09-949-016-12386	Sequence 12386, A
43	33.8	2.4	263694	3	US-09-049-016-16915	Sequence 16915, A
44	33.4	2.4	601	3	US-09-049-016-179331	Sequence 179331, A
45	33.4	2.4	1215	3	US-10-321-188-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-060-756-1
Sequence 1, Application US/09060756
Patent No. 6183957
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMATURES

Result No.	Score	Query			Length	DB	ID	Description
		Match	Length	ID				
1	1407	100.0	12732	3	US-09-060-756-1	X		Sequence 1, Appli
2	1407	100.0	12732	3	US-09-670-314-1	X		Sequence 1, Appli
3	1407	100.0	4411529	3	US-09-103-840-A-2	>X		Sequence 2, Appli
4	1407	100.0	4411529	3	US-09-103-840-A-1			Sequence 1, Appli
C 5	693	49.3	693	3	US-09-894-944-44			Sequence 44, Appli
C 6	427	30.3	498	3	US-09-694-844-43			Sequence 43, Appli
C 7	50.4	3.6	702	3	US-09-143-681A-1167			Sequence 4167, Appli
C 8	39.8	2.8	18037	3	US-09-949-016-13678			Sequence 13678, A
C 9	35.8	2.5	18072	3	US-09-902-540-6354			Sequence 6354, Appli
C 10	35.8	2.5	1583	3	US-09-502-540-408			Sequence 408, Appli
C 11	35.8	2.5	9992	3	US-09-949-016-16832			Sequence 16832, A
C 12	35.8	2.5	8345	3	US-09-949-016-16833			Sequence 16833, A
C 13	35.6	2.5	978	3	US-09-102-540-3161			Sequence 3161, Appli
C 14	35.6	2.5	16350	3	US-09-902-540-1144			Sequence 1144, Appli
C 15	35.4	2.5	601	3	US-09-949-016-177875			Sequence 177875, Appli
C 16	35.4	2.5	1149	3	US-09-252-991A-15594			Sequence 15594, A
C 17	35.4	2.5	1266	3	US-09-252-991A-15752			Sequence 15752, A
C 18	35.4	2.5	44377	2	US-08-804-722C-7			Sequence 7, Appli
C 19	35.4	2.5	44377	2	US-08-804-198-1			Sequence 1, Appli
C 20	35.2	2.5	801	3	US-09-902-540-7819			Sequence 7819, Appli
C 21	35.2	2.5	5147	3	US-09-902-540-780			Sequence 780, Appli
C 22	35	2.5	1215	3	US-10-321-188-72			Sequence 72, Appli
C 23	35	2.5	1215	3	US-10-321-188-72			Sequence 74, Appli
C 24	34.8	2.5	399	3	US-09-621-976-8476			Sequence 8976, Appli
								TYPE : DNA ORGANISM : Mycobacterium tuberculosis US-09-066-756-1

Qy 3.01 CGGGGAGACGTGATGCCGTTAATACTGTTGAACCAAGGATCTACGGTAGTCCAA 360
 Db 3.01 CGGGGAGACGTGATGCCGTTAATACTGTTGAACCAAGGATCTACGGTAGTCCAA 360

Qy 3.61 CTAGAGCCCATAGCCACGCCATTGATGTTGATCGAAAATGGTCCGCATTGACA 420
 Db 3.61 CTAGAGCCCATAGCCACGCCATTGATGTTGATCGAAAATGGTCCGCATTGACA 420

Qy 4.21 TGGCACCACTGGTCAAAGCJAACGTCAGCTGGTTGCGGGTTCAATGACGCCG 480
 Db 4.21 TGGCACCACTGGTCAAAGCJAACGTCAGCTGGTTGCGGGTTCAATGACGCCG 480

Qy 4.81 GCGGTGCGTGCTGAGTTGATGCTGTTAGTAACTGGCACCTCAGCGAGATGGT 540
 Db 4.81 GCGGTGCGTGCTGAGTTGATGCTGTTAGTAACTGGCACCTCAGCGAGATGGT 540

Qy 5.41 CTTGCCCCCTCCGCCATGAAAGTCTACGATTGTTGTCGTCGGTGG 600
 Db 5.41 CTTGCCCCCTCCGCCATGAAAGTCTACGATTGTTGTCGTCGGTGG 600

Qy 6.01 GTCCGAGACTTAACTCTAACAGTGTGCGCGGAAATGACCCAAAAA 660
 Db 6.01 GTCCGAGACTTAACTCTAACAGTGTGCGCGGAAATGACCCAAAAA 660

Qy 6.61 CCGCGCGACGTTGCGAGAAAGCTGGAGAAGTGGAGAATTTCACTGGGA 720
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Qy 7.21 CAGTACCTCAAATAGTCCGAGCCTCCGAGCTTAAGAGAGATCCAGAAATTGAC 780
 Db 7.21 CAGTACCTCAAATAGTCCGAGCCTCCGAGCTTAAGAGAGATCCAGAAATTGAC 780

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 Db 7.81 ACGGCGGCCTGAAACCTTCCCACAAATTGCTTAACTGGCTCATATCGAC 840

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 Db 9.01 GGCCAGAGACATATTGGTCCTGGCCAGGCTTGGCCAGTCTCGTC 960

Qy 9.61 TTGGCGTGGCTATTGTAATTGCCAGAATTGGCAAGTCCGCTGATACGGATAA 1020
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Qy 12.01 ATCTTTGATGAAAAGCTGTCCTCACCTGAGCGGAAAGTCCGCTG 1260
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Qy 13.81 GATTGAAACATCGGACTTTCTTCAC 1407

Db 13.81 GATTGAAACATCGGACTTTCTTCAC 1407

RESULT 2
 US-09-670-314-1
 ; Sequence 1, Application US/09670314
 ; Patent No. 6,925,066
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Stewart
 ; APPLICANT: Buchrieser-Broesch, Roland
 ; APPLICANT: Gordon, Stephen
 ; APPLICANT: Billault, Alain
 ; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
 ; CURRENT FILING DATE: 2001-01-12
 ; PRIORITY NUMBER: US/09/670,756
 ; FILE REFERENCE: 3495-0169
 ; NUMBER OF SEQ ID NOS: 743
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1
 ; LENGTH: 12732
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; US-09-670-314-1

Query	Match	Score	DB	Length
	100 %	1407	3	12732;
	Best Local Similarity	100 %	Pred. No.	0;
	Matches 1407:	Conservative 0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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 Db 1 ACCTGGCTTGGAGATCAAATAGGCGCATGGGTAGCATAGGTGGTGGCCA 60

Qy 61 TCTTGTATGCTGAAATAAGATGTCAGGCAATTAAAGAGAGCAACCTCGG 120
 Db 61 TCTTGTATGCTGAAATAAGATGTCAGGCAATTAAAGAGAGCAACCTCGG 120

Qy 121 CATTCACTGTCGAGSGTTCGATGTCAGGCAACCATTCGGTTCACGATTTCA 180
 Db 121 CATTCACTGTCGAGSGTTCGATGTCAGGCAACCATTCGGTTCACGATTTCA 180

Qy 181 GACGAAGATTGATATTTCACTCGGAGCTGATAGTCGGCTTCGATCTATGGCCCG 240
 Db 181 GACGAAGATTGATATTTCACTCGGAGCTGATAGTCGGCTTCGATCTATGGCCCG 240

Qy 241 CGCAGATGAAACTGCTGCCATTGCGCCACCTTCGAAACCTAGTCGGGGGCCACATT 300
 Db 241 CGCAGATGAAACTGCTGCCATTGCGCCACCTTCGAAACCTAGTCGGGGGCCACATT 300

Qy 3.01 CGGGGAGAGACCTGCAAGCCGENTGTAATCAGTTTGAGGCAAGGGCATCTAGGTAGTC 360
 Db 3.01 CGGGGAGAGACCTGCAAGCCGENTGTAATCAGTTTGAGGCAAGGGCATCTAGGTAGTC 360

Qy 3.61 GTAGAGGCCATTAGCAGCTGTTGCTGATCGAAATGGTCCGGCATTTGCAA 420
 Db 3.61 GTAGAGGCCATTAGCAGCTGTTGCTGATCGAAATGGTCCGGCATTTGCAA 420

Qy 4.21 TCGGCACTAGGCTGTTGCTGATCGCTTCAATGCACTGACGGCGC 480
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Qy 4.81 GGGGGCCGGTGTGCTTGCATGTTGCTGATCACGCGGACCTTCAGCGAGATGGT 540
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Qy 5.41 CGTTGCGCTTTCGCGCATGAGCTGCTCACATTGCTGCTGCTGCTGCTG 600
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Qy 601 GTCCGAGACTATACCTTCAACAGTTCATGCCAGGGCTCGGGGGCAATGACCCAAAA 660
 db 601 GTCCGAGACTATACCTTCAACAGTTCATGCCAGGGCTCGGGGGCAATGACCCAAAA 660
 Qy 661 CCCGCAGGAGCTTCGGCAGAGCGTGGAGCGATAGATAATTCACTGGGA 720
 Db 661 CCCGCAGGAGCTTCGGCAGAGCGTGGAGCGATAGATAATTCACTGGGA 720
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 Db 721 CAGPACCTAAATAGTCCGGCTCGGCTCCGAGCTTAAGGGAGATCCAAATGCA 780
 Qy 781 ACGCGGGGCTCGAACCCPCCCCAACATTGCTTATAATCGGGTAGCCAAAC 840
 Db 781 ACGCGGGGCTCGAACCCPCCCCAACATTGCTTATAATCGGGTAGCCAAAC 840
 Qy 841 CAACTTACCGGAATGCTAAGTTCTCGAACACGGGCTCATCGACATAGGA 900
 Db 841 CAACTTACCGGAATGCTAAGTTCTCGAACACGGGCTCATCGACATAGGA 900
 Qy 901 GGGCCAGAGACATATTCCGCTCGCTGGCCAGGGTTGGCCAAGGAGTTGGCA 960
 Db 901 GGGCCAGAGACATATTCCGCTCGCTGGCCAGGGTTGGCAAGGAGTTGGCA 960
 Qy 961 TTGCGCTGGCTAAATTCTGTAGTCCACAAATTGCGCACTGCGTGTGCGATACCGAGATA 1020
 Db 961 TTGCGCTGGCTAAATTCTGTAGTCCACAAATTGCGCACTGCGTGTGCGATACCGAGATA 1020
 Qy 1021 CTGCAAATTCGCAATTCAATAGACCGCTGTGAGTAAGGAAGATTGCGCTGTCTTG 1080
 Db 1021 CTGCAAATTCGCAATTCAATAGACCGCTGTGAGTAAGGAAGATTGCGCTGTCTTG 1080
 Qy 1081 AGTTAAATGGCCGGAGCCAGTCAGCGATCTCGGAAATAATGACGGGGCGCTGTAGTTG 1140
 Db 1081 AGTTAAATGGCCGGAGCCAGTCAGCGATCTCGGAAATAATGACGGGGCGCTGTAGTTG 1140
 Qy 1141 AATTCTACTGCCGCCACTGCGCTTCCCAATCTGGTGGCCGATCAAGCGCTCTCACGT 1200
 Db 1141 AATTCTACTGCCGCCACTGCGCTTCCCAATCTGGTGGCCGATCAAGCGCTCTCACGT 1200
 Qy 1201 ATCTTTGATGGAAACGTCGCTTCACTCTGACGGAAACGTTATCCACTGTAACCCCTGG 1260
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 Qy 1261 CTGCTTGTGATCGGATTCTGCAATCAGCTGTTGCAATCAGCTGTTGATCATCATAG 1320
 Db 1261 CTGCTTGTGATCGGATTCTGCAATCAGCTGTTGCAATCAGCTGTTGATCATCATAG 1320
 Qy 1321 ATGATGAATTCATGCCGAAATTCCTCGCCAAGGGATGTGTAATT 1380
 Db 1321 ATGATGAATTCATGCCGAAATTCCTCGCCAAGGGATGTGTAATT 1380
 Qy 1381 GATTGAACATCGGACTATGCCGAAATTCCTGCCGAAAGGATGTGTAATT 1407
 Db 1381 GATTGAACATCGGACTATGCCGAAATTCCTGCCGAAAGGATGTGTAATT 1407
 RESULT 3
 US-09-103-810A-2
 Sequence 2, Application US/09103840A
 Patent No. 6294328
 GENERAL INFORMATION:
 APPLICANT: FLEISCHMAN, Robert D.
 APPLICANT: WHITE, Owen R.
 APPLICANT: FRASER, Claire M.
 APPLICANT: VENTER, John C.
 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 TITLE OF INVENTION: TUBERCULOSIS
 FILE REFERENCE: 24336-26007.00
 CURRENT APPLICATION NUMBER: US/09/103, 840A
 CURRENT PILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1

RESULT 5
US-09-894-844-44/c
Sequence 44, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894, 844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/31B, 191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097, 936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
; SEQ ID NO 44 :
US-09-894-844-44

Query Match Score 49.3%; Score 693; DB 3; Length 693;
Best Local Similarity 100.0%; Pred. No. 4.9e-216;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1697215 ATCTTGTGATGAAACGGTCACTGGAACTGGTACCCCTGG 1697274
Qy 1261 CTCGTTTGTGATCGATTCTGTTGCCATAACGGTGTGATATTGATCATAG 1320
Db 1697275 CTCGTTTGTGATCGATTCTGTTGCCATAACGGTGTGATATTGATCATAG 1697334
Qy 1321 ATGATGATTACATCGACGAAATGATCCTGCCAAGGTATGTAATT 1380
Db 1697335 ATGATGATTACATCGACGAAATGATCCTGCCAAGGTATGTAATT 1697394
Qy 1381 GATTGAAATCGGACTTTCTCAAC 1407
Db 1697395 GATTGAAATCGGACTTTCTCAAC 1697421

RESULT 6
US-09-894-844-43/c
Sequence 43, Application US/09894844
; Sequence 43, Application US/09894844
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894, 844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/31B, 191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097, 936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
; SEQ ID NO 43 :
US-09-894-844-43

Query Match Score 30.3%; Score 427; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.5e-129;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 693 CTGGCAGCATCTAAATAGCTGGGCTCTGGCTAACAGGAGATCCAG 634
Qy 774 ATCGACAGGGGGCTGAACCTCCCCAACATTGCTTATAATCGGGTAGCGTCATA 833
Db 633 ATCGACAGGGGGCTGAACCTCCCCAACATTGCTTATAATCGGGTAGCGTCATA 574
Qy 834 ATCGAACCAAGTACCCGATGCTAAGTCTGTTGAAACACGGCTCATCGAACG 893
Db 573 ATCGAACCAAGTACCCGATGCTAAGTCTGTTGAAACACGGCTCATCGAACG 514
Qy 894 GGCTGAAGGGCAAGAGACATATCGGTGCTGGCCCTGTCAGACGCTGCCAGCT 953
Db 513 GGCTGAAGGGCAAGAGACATATCGGTGCTGGCCCTGTCAGACGCTGCCAGCT 454
Qy 954 CTGGCTCTGGCTGCTTAATCGTAGTCCTAACAGGAATTGGCAAGTGGCTGTGATACC 1013
Db 453 CTGGCTCTGGCTGCTTAATCGTAGTCCTAACAGGAATTGGCAAGTGGCTGTGATACC 394
Qy 1014 GGATAACTGCAAATGATCATATGAGGCTGTTGAGAAGACATCTGTGTG 1073
Db 393 GAGATAACTGCAAATGCTTAATGAGGCTGCTGTTGAGAAGACATCTGTGTG 334
Qy 1074 TCTCTCAGGTAATCGCGGAACTCGGATCTCCGAAATCGGCCCACGCT 1133
Db 333 TCTCTCAGGTAATCGCGGAACTCGGATCTCCGAAATCGGCCCACGCT 274

Db 273 CTGATGTAATCTGCTAGTGCCTGCTGATCGGTAACTGGCT 214
Qy 1194 CTCACTGATCTCTTGTGATGGAAAACCTCCCTCACCTGACGGAAACAGTTATCCACTGTAA 1253
Db 213 CTCACTGATCTCTTGTGATGGAAAACCTCCCTCACCTGACGGAAACAGTTATCCACTGTAA 154
Qy 1254 CCCCTGGCTGCTGTTGATCGATTCTGTTGCGCATACGCGTTGTTGATATGGCTGTC 1313
Db 153 CCCCTGGCTGCTGTTGATCGATTCTGTTGCGCATACGCGTTGTTGATATGGCTGTC 94
Qy 1314 ATCATGATGATGATGATCATCGACGAAATCGGATCAATCGCTGCCAAAGGTAT 1373
Db 93 ATCATGATGATGATCATCGACGAAATCGGATCAATCGCTGCCAAAGGTAT 34
Qy 1374 GTAAATTGATTGACAAATCGGGAATCTGCTTCTCAA 1406
Db 33 GTAAATTGATTGACAAATCGGACTTCTCAA 1

Db 1134 GTATGTTGAAATTCTGTCGGCCAGTGCCTTCCCAATCGGTTCCGCTGCGGT 1193

RESULT 7
US-09-543-681A-4167/C
; Sequence 4167, Application US/09543681A
; Patent No. 6607509
GENERAL INFORMATION:
; APPLICANT: GARY BRATON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TYPE: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQ ID NOS: 8344
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; SEQ ID NO 4167
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4167

Query Match 2.8%; Score 39.8; DB 3; Length 18037;
Best Local Similarity 48.1%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 113; Conservative 122; Mismatches 0;

Qy 411 GCGATTGCAATTCGGCACCAGGTGGTAAAGGCCAACCCCTGCCGCTTCGCCTGCAA 470
Db 3848 GCCTAAGGCCCTCGCCAGCTGACCAAGCGGGCACCTGCCGCTTGAGCCCTGCCAG 3907

Qy 471 TCGACGCCGGCGGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 530
Db 3908 GTGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAG 3967

Qy 531 CGAGCATGGTGTGTTGCTTCGCTTCGCTTCGCTTCGATGAAGCTGCTCACGATTCGCGCT 590
Db 3968 AGTGCCTGTTCTCCACAGTGTAGGGCGAGCTACAGGGTGTAGGGCGGGCGGG 4027

RESULT 9
US-09-902-540-6354/C
; Sequence 6354, Application US/09902540
; Patent No. 6833447
GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10/15849/B
; CURRENT APPLICATION NUMBER: US/09/902, 540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217, 883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 168255
; SEQ ID NO 6354
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6354

Query Match 2.5%; Score 35.8; DB 3; Length 702;
Best Local Similarity 56.3%; Pred. No. 0.55; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 52;

Qy 203 CGCGAACCTATAAGTCGCCCTCCGCGACTATGCGGCCGAGATGAGTCGCTGCTTGC 262
Db 225 CGCGTCCAAACGACTCCGGCGCGGATGCGGCCGCTCCGAGATGCGGCCGAGGGCTCC 166

Qy 263 CGGACCTTCGAAACGATGCTAGTACGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 321
Db 165 CAGCCGCTCCTAGAACACCGGGCGGCCCTCCCTGGAGAAGAGCGGATGG 107

RESULT 10
US-09-902-540-408/C
; Sequence 408, Application US/09902540
; Patent No. 6833447
GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10/15849/B
; CURRENT APPLICATION NUMBER: US/09/902, 540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217, 883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 168255

RESULT 8
US-09-949-016-13678
; Sequence 13678, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLJ001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/1241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13678
; LENGTH: 18037
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13678

SEQ ID NO 408
; LENGTH: 1583
; TYPE: DNA.
; ORGANISM: Myxococcus xanthus
; US-09-902-510-408

Query Match 2.5%; Score 35.8; DB 3; Length 1583;
Best Local Similarity 56.3%; Pred. No. 0.87;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 203 CGGACGGTATACTCCGCATTAATGCCGCCAGATGAGAGTCCTCGCTTCG 262
Db 1106 CGGGTCGAAGCAGACTCCGCTCCGGAAAGTAGCGCCTCCACAGAGGGTCTC 1047
Qy 263 CCCACUTTGAAACGTAGTGCACCGGGCAATTGGGGAGACGTGATGCCG 321
Db 1046 CAAGCGCTCTCGACACACCGGGCGGGCTCTGGAGAGGGATGG 988

RESULT 11
US-09-949-016-16832/c
Sequence 16832, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16832
LENGTH: 5992
TYPE: DNA.
ORGANISM: Human
US-09-949-016-16832

Query Match 2.5%; Score 35.8; DB 3; Length 5992;
Best Local Similarity 51.1%; Pred. No. 1.8; Mismatches 102; Indels 6; Gaps 1;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

Qy 75 GAATAAGATGTCAGGCAATTAAAAGAGAACGCCAACGGGCAATTCAGCATGTCG 134
Db 3344 GACGAAAGCTGGGTCAACACAGGCCAACAGGCAAGGGGCAATCTAAGGAC 3285
Qy 135 AGGTCTGGTCCA-----TGTGAGCGCAACATTCCGGCACAGATTCAAGCA 188
Db 3284 ACAGTCGATCCAGGGTCACTGCACTGACCTGACCCACCTCACTGAGA 3225
Qy 189 TGTAAATACTCCACCTGCGCACTAGTCGCTCGATCTATGCCGCCGAGATG 248
Db 3224 TGTAAACCCCTCTGGAGAACCTGATCGCCACCTACAGCCCCGAGGTACT 3165
Qy 249 AAGTCCTGGTGGCCGACATTCGAAACGTAGTGCGGCCGC 289
Db 3164 GGCCCTGGCCCGCACTGGCCGCTGTC 3124

RESULT 12
US-09-949-016-16833
Sequence 16833, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16833
LENGTH: 8345;
Query Match 2.5%; Score 35.8; DB 3; Length 8345;
Best Local Similarity 51.1%; Pred. No. 2.2; Mismatches 102; Indels 6; Gaps 1;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

Qy 75 GATAAGATGTCAGGCAATTAAAAGAGAACGCCAACGGGCAATTCAGCATGTCG 134
Db 6980 GAGGAACCTGGTCAACAGGGCAAGAGGGGATCTAAGTGGAC 7039
Qy 135 ACGCTCGCTTCA-----TGTGAGGCACATTCCGTGTCACGATTCAAGGACA 188
Db 7040 ACAGTCGATCCAGGGTCACTGACCTGACCCACCTACAGGCTGAGCTGAGA 7099
Qy 189 TGTAAATACTCCACCTGGCACGTATAGTCGGCTCCGATCTATGCCGCCGAGATG 248
Db 7100 TGAAAGCCCTCTGGAGAACCTGATCCGCCCCACCTACAGGCCCGAGGTACT 7159
Qy 249 AAGTCCTGGTGGCCGACCTTCGAAACGTAGTGCGGCCGC 289
Db 7160 GGCCCTGGCCGACACCTTGGCCGAGTGGCTCTGTC 7200

RESULT 13
US-09-902-540-3161/c
Sequence 3161, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3161
LENGTH: 978
TYPE: DNA.
ORGANISM: Myxococcus xanthus
US-09-902-540-3161

Query Match 2.5%; Score 35.6; DB 3; Length 978;
Best Local Similarity 57.0%; Pred. No. 0.77; Mismatches 0; Indels 0; Gaps 0;

Qy 215 GTCCGCTCCGATCTGATGGCGGAGATGAGCTGGCTTCCCGACCTTCGAA 274
Db 531 GTCCGCTTGGCTTCGCTTCGCTTCAACAGGGCAATGAGCTGGCTTCCGCGGCAC 472
Qy 275 ACGTATGTCGACCTGGGGCACTTGGGGAGACCTGATGCGCTGATTC 328
Db 471 CTGCAACGCCGCGCTGGCCACCTCCGCGACCATGGACCATGGCTCTC 418

RESULT 14
US-09-902-540-1144
; Sequence 1.144, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1144
; LENGTH: 16350
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-1144

Query Match 2.5%; Score 35.6; DB 3; Length 16350;
Best Local Similarity 57.0%; Pred. No. 3.8;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy 215 GTGGCCCTCCGCAATCTATGGCGGCCAGATGAAGTCTGGTTGCCACCTTGAA 274
Db 3602 GTTCGCCTTGCCTCCTGCCTCACACGGGTGACGGGTGCTGGCGGCCAAC 3661

Qy 275 ACCTAGTGGCGCGCGCACCAATTGGGGAGAGCTGATGCCGTGATACTC 328
Db 3562 CTGACCGCGCGGTGCACCGCTCCGGCATGGACACGAGCTCT 3715

RESULT 15
US-09-949-016-177875
; Sequence 1.77875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/03/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 177875
; LENGTH: 6,01
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-177875

Query Match 2.5%; Score 35.4; DB 3; Length 601;
Best Local Similarity 50.7%; Pred. No. 0.68;
Matches 112; Conservative 1; Mismatches 102; Indels 6; Gaps 1;
Qy 75 GAATAAGATGTCAGGGAAATTAAAAGAGAAGGCCAACGGGAATCTGGCATGTCG 134
Db 218 GAGGAAGTGGGTCAACACAGGCCAACAGGGGAAGGGGATTAACTAGGAC 277

Qy 135 AGGTGCTCTCA-----TGTGAGCCGCACATTCCCTGTCACATTGAGCAACA 188
Db 278 ACAGTCCGATCCAGGGCTCACTCRCCCTGACCCACCTTGACTGAGA 337

Qy 189 TGAATAATTCCACACTGCGAGCTATAGTCGCGCTCCGATCTATGCGCGCGAGATG 248

Result No.	Score	Query Match	Length	DB ID	Description
1	1407	100.0	1232	6	US-10-259-678-1
c 2	693	49.3	693	3	Sequence 1, Appli
c 3	693	49.3	693	7	Sequence 44, Appli
c 4	693	49.3	693	7	Sequence 44, Appli
c 5	427	30.3	498	3	Sequence 44, Appli
c 6	427	30.3	498	7	Sequence 44, Appli
c 7	427	30.3	498	7	Sequence 44, Appli
c 8	39.8	2.8	27204	5	Sequence 1528, Appli
c 9	38.4	2.7	2464	9	Sequence 1, Appli
c 10	37.8	2.7	536	7	Sequence 44, Appli
c 11	37.8	2.7	894	6	Sequence 44, Appli
c 12	37.8	2.7	9025608	6	Sequence 1933, Appli
c 13	36.6	2.6	485	7	Sequence 1, Appli
c 14	36.2	2.6	783	6	Sequence 48583, Appli
c 15	36	2.6	126	7	Sequence 2972, Appli
c 16	36	2.6	1188	8	Sequence 34546, Appli
c 17	35.8	2.5	17138	8	Sequence 62490, Appli
c 18	35.6	2.5	1662	7	Sequence 1009, Appli
c 19	35.4	2.5	622	4	Sequence 597843, Appli
c 20	35.4	2.5	727	9	Sequence 3059, Appli
c 21	35.4	2.5	727	9	Sequence 8294, Appli
c 22	35.4	2.5	1632	6	Sequence 44333, Appli
c 23	35.4	2.5	4698	6	Sequence 6923, Appli

Db	1321	ATGATGAATTATCGAGAAATCGCAATTCAGGTCAAATATCCCTGCCAAGGTATGTAAATT	1380
Qy	1381	GATTGACAAATCGGGTTTCTTCAC	1407
Db	1381	GATTGACAAATCGGGTTTCTTCAC	1407
Qy			RESULT 2
Db	US-09-894-844-44/c		
	Sequence 44 , Application US/09894844		
	Patent No. US20020176873A1		
Qy			GENERAL INFORMATION:
Db			APPLICANT: Behr, Marcel
Qy			APPLICANT: Small, Peter
Db			APPLICANT: Schoonik, Gary A.
Qy			APPLICANT: Wilson, Michael A.
			TITLE OF INVENTION: Molecular Differences Between Species of
			TITLE OF INVENTION: the M. Tuberculosis Complex
			FILE REFERENCE: STAN102CON
			CURRENT APPLICATION NUMBER: US/09/894,844
			CURRENT FILING DATE: 2001-06-27
			PRIOR APPLICATION NUMBER: 09/318,191
			PRIOR FILING DATE: 1999-05-25
			PRIOR APPLICATION NUMBER: 60/097,936
			PRIOR FILING DATE: 1998-08-25
			NUMBER OF SEQ ID NOS: 137
			SOFTWARE: FastSEQ for Windows Version 4.0
			SEQ ID NO: 44
			LENGTH: 693
			TYPE: DNA
			ORGANISM: Mycobacteria tuberculosis
			US-09-894-844-44
			Query Match 49.1%; Score 693; DB 3; Length 693;
			Best Local Similarity 100.0%; Pred. No. 3.7e-227;
			Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	714	CTGGCACAGAACCTCAAATAGTCCCAGCCCTCGAGCTAAAGAGCAGATCCAGAAC	773
Db	693	CTGGCACAGAACCTCAAATAGTCCCAGCCCTCGAGCTAAAGAGCAGATCCAGAAC	634
Qy	774	AATCGAACAGGGGGCTCGAACCCCTCCCACAAATGCTTAAATCGGGTAGCCGTATA	833
Db	633	AATCGAACAGGGGGCTCGAACCCCTCCCACAAATGCTTAAATCGGGTAGCCGTATA	574
Qy	721	CAGTACCTCAAATAGTCGGACGAGCTCCGACCTTAAGAGCAGATCCAGAAC	780
Db	721	CAGTACCTCAAATAGTCGGACGAGCTCCGACCTTAAGAGCAGATCCAGAAC	780
Qy	781	ACGGGGGGCTCGAACCCCTCCCACAAATTGCTTAAATCGGGTAGCCGTATAATCGAAC	840
Db	781	ACGGGGGGCTCGAACCCCTCCCACAAATTGCTTAAATCGGGTAGCCGTATAATCGAAC	840
Qy	841	CAAGTTACCGGATGTAAGTTGTCGAAACACGGCTCATCGAACATAGAACGGCTGAG	900
Db	841	CAAGTTACCGGATGCTAGTTGTCGAAACGGCTCATCGAACATAGAACGGCTGAG	900
Qy	901	GGGCCAGAGACATAATTGGTCGCTCGGGCCTTTGGCAAGAGCTTGCCCATCTCGGT	960
Db	901	GGGCCAGAGACATAATTGGTCGCTCGGGCCTTTGGCAAGAGCTTGCCCATCTCGGT	960
Qy	961	TTCGCCCTGGCTTAATTCGCTGCTCCACGAAATTGCCAGTCCGCTGATACCAGATAA	1020
Db	961	TTCGCCCTGGCTTAATTCGCTGCTCCACGAAATTGCCAGTCCGCTGATACCAGATAA	1020
Qy	1021	CTGCAAATTCGCAATTCAATAGACGCCATTGGCTGCTGTTCTTCG	1080
Db	1021	CTGCAAATTCGCAATTCAATAGACGCCATTGGCTGCTGTTCTTCG	1080
Qy	1081	AGTTAAATCGGGCGAGCCATTGGCTGCTCCACGATTCGCCGCGCCTGTAGTTG	1140
Db	1081	AGTTAAATCGGGCGAGCCATTGGCTGCTCCACGATTCGCCGCGCCTGTAGTTG	1140
Qy	1141	AATTCTAGTGCCTGGCTTAATCGCAAAATTGCGCTTGGCTCGATCAAGCT	1200
Db	1141	AATTCTAGTGCCTGGCTTAATCGCAAAATTGCGCTTGGCTCGATCAAGCT	1200
Qy	1201	CTGCTTGTGTCGAACTCGCACTCGCTTGGCTCGATCACTGCACTGCACTG	1260
Db	1201	CTGCTTGTGTCGAACTCGCACTCGCTTGGCTCGATCACTGCACTGCACTG	1260
Qy	1261	CTGCTTGTGTCGAACTCGCACTCGCTTGGCTCGATCACTGCACTGCACTG	1320
Db	1261	CTGCTTGTGTCGAACTCGCACTCGCTTGGCTCGATCACTGCACTGCACTG	1320
Qy	1321	ATGATGAATTATCGAGAAATGCAATCGGTCAAATATCTCGCCAAGGTTAATT	1380
Db	213	CTOACGATCATCGAGAAATGCAATCGGTCAAATATCTCGCCAAGGTTAATT	154

Qy	1254	CCCTGGGCTGGTTGATCGAATTCTGCCAAATCACTGGTGTGATATTGCACTGTC	1313	Qy	1134	GTAGTTGAATTCTGGTTGATCGCAGTGCCTTCGGCCATGCTGGCCCTGGATAGGGT	1193
Db	153	CCCTGGGCTGGTTGATCGAATTCTGCCAAATCACTGGTGTGATATTGCACTGTC	94	Db	273	GTAATTGAACTTCTGGCTGATGCTGATGCTGATGCTGATGCTGATGCT	214
Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373	Qy	1194	CTCACTGATCTTGTGATGAAAAGCTCCCTCACTGGACGGAAAGGTATCCACTGTAA	1253
Db	93	ATCATAGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34	Db	213	CTCACTGATCTTGTGATGAAAAGCTCCCTCACTGGACGGAAAGGTATCCACTGTAA	154
Qy	1374	GTAATTGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406	Qy	1254	CCCTGGGCTGGTTGATCGATTCTGTTTCGCAATACAGCTTGATATTGCACTGTC	1313
Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1	Db	153	CCCTGGGCTGGTTGATCGATTCTGTTTCGCAATACAGCTTGATATTGCACTGTC	34
RESULT 3				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
US-10-388-902-44/C				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; Sequence 44, Application US/10388902				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; GENERAL INFORMATION:				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; APPLICANT: Behr, Marcel				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; APPLICANT: Small, Peter				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; APPLICANT: Schoolnik, Gary				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; APPLICANT: Wilson, Michael A.				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
RESULT 4				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
US-10-647-089-44/C				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; Sequence 44, Application US/10647089				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; Publication No. US20040063923A1				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; GENERAL INFORMATION:				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; APPLICANT: Behr, Marcel				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; APPLICANT: Small, Peter				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; APPLICANT: Schoolnik, Gary				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; APPLICANT: Wilson, Michael A.				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; TITLE OF INVENTION: Molecular Differences Between Species of				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; TITLE OF THE M. Tuberculosis Complex				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; FILE REFERENCE: STAN102CON				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; CURRENT APPLICATION NUMBER: US/10/388,902				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; CURRENT FILING DATE: 2003-03-14				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; PRIOR APPLICATION NUMBER: US/09/894,844				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; PRIOR FILING DATE: 2001-06-27				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; PRIORITY NUMBER: 09/3118,191				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; PRIORITY FILING DATE: 1999-05-25				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; PRIORITY NUMBER: 60/097,936				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; NUMBER OF SEQ ID NOS: 137				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; SOFTWARE: FastSEQ for Windows Version 4.0				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; SEQ ID NO: 44				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; LENGTH: 693				Qy	1374	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; TYPE: DNA				Db	33	GTATTGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	34
; ORGANISM: Mycobacteria tuberculosis				Qy	1314	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1373
; US-10-388-902-44				Db	93	ATCATAGATGATGAAATTCACTGACGAATGCAATTAGGTCAAATAATCCTGCCAAGGTAT	1406
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	714	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	773
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; SEQ ID NO: 44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; LENGTH: 693				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; TYPE: DNA				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; ORGANISM: Mycobacteria tuberculosis				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; US-10-647-089-44				Qy	714	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	773
; Query Match 49.3%; Score 693; DB 7; Length 693;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; SEQ ID NO: 44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; LENGTH: 693				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; TYPE: DNA				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; ORGANISM: Mycobacteria tuberculosis				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; US-10-647-089-44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; SEQ ID NO: 44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; LENGTH: 693				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; TYPE: DNA				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; ORGANISM: Mycobacteria tuberculosis				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; US-10-647-089-44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; SEQ ID NO: 44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; LENGTH: 693				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; TYPE: DNA				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; ORGANISM: Mycobacteria tuberculosis				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; US-10-647-089-44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; SEQ ID NO: 44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; LENGTH: 693				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; TYPE: DNA				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; ORGANISM: Mycobacteria tuberculosis				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; US-10-647-089-44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; SEQ ID NO: 44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; LENGTH: 693				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; TYPE: DNA				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; ORGANISM: Mycobacteria tuberculosis				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; US-10-647-089-44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; SEQ ID NO: 44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; LENGTH: 693				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; TYPE: DNA				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; ORGANISM: Mycobacteria tuberculosis				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; US-10-647-089-44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; SEQ ID NO: 44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; LENGTH: 693				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; TYPE: DNA				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; ORGANISM: Mycobacteria tuberculosis				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; US-10-647-089-44				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; SEQ ID NO: 44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; LENGTH: 693				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; TYPE: DNA				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; ORGANISM: Mycobacteria tuberculosis				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; US-10-647-089-44				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	693
; Best Local Similarity 100.0%; Pred. No. 3.7e-227;				Qy	774	AATGCGAACAGCCGGCTCGAACCCCTCCCCAACATTGCTTATAATCGCGCTTAAAGGAGCATCCAG	833
; Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Db	693	CTGGCGACAGTACCTCAAAATAGTCCGGAGCCCTCGGCTTAAAGGAGCATCCAG	

Qy 1014 GAGATAACTGCAATTCAAATAGACGCCCTGTAGTAAAGAAAGATTGGTGTGTCCT 1073
 Db 393 GAGATAACTGCAATTCAAATAGACGCCCTGTAGTAAAGAAAGATTGGTGTGTCCT 334
 Qy 1074 TTCTTCGAGGTAAATATCGGCCGCACTCAGGGATCTCCGCCAAATAGACGCCCTGTGCTG 1133
 Db 333 TTCTTCGAGGTAAATATCGGCCGCACTCAGGGATCTCCGCCAAATAGACGCCCTGTGCT 274
 Qy 1134 CTAGTTGATTTTACTGCCCCCAATCGGCCCTTGCTGCTGCTGCTGCTGCTGCTGCT 1193
 Db 273 CTAGTTGATTTACTGCCCCCAATCGGCCCTTGCTGCTGCTGCTGCTGCTGCTGCT 214
 Qy 1194 CTCACGATTCATTTGATGAAAAGTCCTCTTACCTGCAAGGAAACAGTTATCCTGTA 1253
 Db 213 CTACGATTCATTTGATGAAAAGTCCTCTTACCTGCAAGGAAACAGTTATCCTGTA 154
 Qy 1254 CCCCTGGCTCGTTTGATCGATTCTGCCTTCGCCAATACACGCTTGTTGATGTC 1313
 Db 153 CCCCTGGCTCGTTTGATCGATTCTGCCTTCGCCAATACACGCTTGTTGATGTC 94
 Qy 1314 ATCATAGATGATGATTCATCGATTCTGCCTTCGCCAATACACGCTTGTTGATGTC 1373
 Db 93 ATCATAGATGATGATTCATCGATTCTGCCTTCGCCAATACACGCTTGTTGATGTC 34
 Qy 1374 GAAATTGATGACAATCGGACTATCTCA 1406
 Db 33 GAAATTGATGACAATCGGACTATCTCA 1
 RESULT 5
 US-09-894-844-43/c
 ; Sequence 43, Application US/09894844
 ; Patent No. US/09/020176972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behr, Marcel
 ; APPLICANT: Small, Peter
 ; APPLICANT: Schoolnik, Gary
 ; APPLICANT: Wilson, Michael A.
 ; TITLE OF INVENTION: Molecular Differences Between Species of
 ; TITLE OF INVENTION: M. Tuberculosis Complex
 ; FILE REFERENCE: STAN102CON
 ; CURRENT FILING DATE: 2003-03-14
 ; PRIORITY NUMBER: US/09/894,844
 ; PRIORITY FILING DATE: 2001-06-27
 ; PRIORITY NUMBER: US/09/318,191
 ; PRIORITY FILING DATE: 1999-05-25
 ; PRIORITY NUMBER: 60/097,936
 ; PRIORITY FILING DATE: 1998-08-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 498
 ; TYPE: DNA
 ; ORGANISM: Mycobacteria tuberculosis
 ; US-10-388-902-43
 Query Match 30.3%; Score 427; DB 3; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.3e-135; Mismatches 0; Indels 0; Gaps 0;
 Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ACCTGCGCTTGGAGAGATCAAATAGGGCCATGGTAGCATAGGTGCTGGCA 60
 ; CURRENT APPLICATION NUMBER: STAN102CON
 ; CURRENT FILING DATE: 2001-06-27
 ; PRIORITY NUMBER: 60/097,936
 ; PRIORITY FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 498
 ; TYPE: DNA
 ; ORGANISM: Mycobacteria tuberculosis
 ; US-09-894-844-43
 Query Match 30.3%; Score 427; DB 3; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.3e-135; Mismatches 0; Indels 0; Gaps 0;
 Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 61 TCTTTGATGATGGAAATAAGATGTCAGGCAATTAAAGAGAACGCACTCTGGCG 120
 Db 367 TCTTTGATGATGGAAATAAGATGTCAGGCAATTAAAGAGAACGCACTCTGGCG 308
 Qy 121 CATTCAAGCAATGTCAGGCAATGGTAGCATGGTCAAGGTTGCTGGCA 180
 Db 427 ACCTGCGCTTGGAGAGATCAAATAGGGCCATGGTAGCATGGTCAAGGTTGCTGGCA 368
 Qy 61 TCTTTGATGATGGAAATAAGATGTCAGGCAATTAAAGAGAACGCACTCTGGCG 120
 Db 367 TCTTTGATGATGGAAATAAGATGTCAGGCAATTAAAGAGAACGCACTCTGGCG 308
 Qy 121 CATTCAAGCAATGTCAGGCAATGGTAGCATGGTCAAGGTTGCTGGCA 180
 Db 427 ACCTGCGCTTGGAGAGATCAAATAGGGCCATGGTAGCATGGTCAAGGTTGCTGGCA 368
 Qy 61 GAGGAACATGGAAATAATCCACCTCGGAGCTATAGTCGGCTCCGATCTATGGTGTG 188
 Db 307 CATTCAAGCAATGTCAGGTCAGTGTGAGGTGCTGGTAGCTGGGCGACATT 248
 Qy 181 GAGGAACATGGAAATAATCCACCTCGGAGCTATAGTCGGCTCCGATCTATGGTGTG 240
 Db 247 GAGGAACATGGAAATAATCCACCTCGGAGCTATAGTCGGCTCCGATCTATGGTGTG 188
 Qy 241 CCCAGATGAACTGCTGGCTTCCGCAACCTCTGGCACTCTGGCACTCTGGCG 300
 Db 187 CGCAGATGAACTGCTGGCTTCCGCAACCTCTGGCACTCTGGCACTCTGGCG 128
 Qy 301 CGGGGAGACCTCGTCAACTCGGCTCCGATCTATGGTGTG 360

Best Local Similarity 48.6%; Pred. No. 0.22; Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

NAME/KEY: misc feature
LOCATION: (273) .. (273)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (347) .. (347)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (357) .. (357)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (398) .. (398)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (419) .. (419)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (509) .. (509)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: (517) .. (517)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc feature
LOCATION: US-10-338-110-119

Query Match 2.7%; Score 37.8; DB 7; Length 536;

Best Local Similarity 10.0%; Pred. No. 0.16; Gaps 0;

Matches 33; Mismatches 128; Indels 0;

GENERAL INFORMATION

APPLICANT: Fuhrmann, Jeffrey J.

APPLICANT: Romesser, James A.

TITLE OF INVENTION: A Method To Assess Quorum Sensing Potential Of Microbial Communities

CURRENT APPLICATION NUMBER: US/10/338,110

FILE REFERENCE: HRR-0036

CURRENT FILING DATE: 2003-01-07

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Parent in version 3.2

SEQ ID NO: 119

LENGTH: 536

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Consensus Sequence

FEATURE: NAME/KEY: misc_feature
LOCATION: (7) .. (7)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc_feature
LOCATION: (21) .. (21)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc_feature
LOCATION: (33) .. (33)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc_feature
LOCATION: (69) .. (69)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc_feature
LOCATION: (87) .. (87)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc feature
LOCATION: (213) .. (213)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc feature
LOCATION: (226) .. (226)

OTHER INFORMATION: n is a, c, g, or t

FEATURE: NAME/KEY: misc feature
LOCATION: (261) .. (261)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

RESULT 11

US-10-156-761-1933/C

Sequence 1933, Application US/10156761

GENERAL INFORMATION

Publication No. US20030119018A1

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIGAWA, HIROSHI

APPLICANT: SHIBA, TADASHI

APPLICANT: SAKAKI, YOSHITAKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

US-10-437-963-4583
; Sequence 48583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53221)B
; CURRENT APPLICATION NUMBER: US/10437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 48583
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(894)
; SEQ ID NO 1933
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(894)
; SEQ ID NO 1933
; LENGTH: 894;
; Score 37.8; DB 6; Length 894;
; Best Local Similarity 61.9%; Pred. No. 0.21; Indels 0; Gaps 0;
; Matches 60; Conservative 0; Mismatches 37; DB
; Qy 403 GCTCCGGCATTTGACATGTGCACCACTGGTCAAAGGCCAACGCCCTTCTGC 462
; Db 192 GGCGCGATGCGGGAGACAGCAGCACAGTCAGTGGCCGGCACAGGGGCCAGCTTG 133
; Qy 463 CCGTCCAAATCGACGCCGGGGTGTGTGTCTCG 499
; Db 132 CGTCGCCTTCGTCGTCGGGGCTGATCGGGCTCTCG 96
; Db
; RESULT 12
; US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, TUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAI, YOSHITAKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
; SEQ ID NO 1933
; LENGTH: 894;
; Score 37.8; DB 6; Length 894;
; Best Local Similarity 61.9%; Pred. No. 22;
; Matches 60; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
; Qy 403 GCTCCGGCATTTGACATGTGCACCACTGGTCAAAGGCCAACGCCCTTCTGC 462
; Db 2380428 GGCGCGATGCGGGAGACAGCAGTCAGTGGCCGGCTGCTG 2380428
; Qy 463 CGTTCCAAATCGACGCCGGGGTGTGTGTCTCG 499
; Db 2380488 CGTCGCCTTCGTCGTCGGGGCTGATCGGGCTCTCG 2380524
; RESULT 14
; US-10-156-761-2972/c
; Sequence 2972, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAI, YOSHITAKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; RESULT 15

CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIORITY NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 2972
 LENGTH: 783
 TYPE: DNA
 FEATURE:
 ORGANISM: Streptomyces avermitilis
 NAME/KEY: CDS
 LOCATION: (1)..(783)
 us-10-156-761-2972

Query Match Score 36.2; DB 6; Length 783;
 Best Local Similarity 50.9%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 86; Conservative 0; Mismatches 83;

Qy	221	CTCCCCGATCATTCGGCGCCGAGACAGCTGCCTTGCCTGGCCGACCTCCAAACGTCAG
Dy	342	CTCGGGGTCCTTCAGTCGCTGGCGCTGCGAAGAACGGCTGTCGCCAACCTGCC
Qy	281	TGGGGCCCGGGCACATTTCGGGGAGAGTGATCGGTGAATCTGTTGAGGC
Dy	282	CTCGGGATGGTCAAGCAGGGGGTCAGGGTGACGCCGGTCTGTCGCTTCGGAG
Qy	341	ACCGGCATCTAGTAGTCAGTCAGTAGAGGCCATAGCCACAGCTAGATCG
Dy	222	ACGGCGAGCAGGGCGTGTGGTCCCGTGCAGGGGAGGTG

Score 36.2; DB 7; Length 1126;
 Best Local Similarity 56.9%; Pred. No. 1; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 50;

Qy 447 GCTGCGCGGCTTCGCGCTTCCATCGACGCCGCGCGCTGCGCTTGAGTTTCG
 Dy 675 GCGCGCAAGGGCTCGCGAGGCCATCGAGCCGCTTACCGCGAGGGG
 Qy 507 ATGGTGTAGTAACGGCCAAGTCAGGGGATGATGTTGCTTCGCGCATGAG
 Dy 735 AGCCCGAGGCTGCGCTGAGCTGCGGAAACTGCGCGCTGCGCATGAG

RESULT 15
 US-10-425-114-34546
 Sequence 34546, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 34546
 LENGTH: 1126
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: UC-ZMFLM017285A04_FLI
 us-10-425-114-34546

Query Match Score 36.2; DB 7; Length 1126;
 Best Local Similarity 56.9%; Pred. No. 1; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 50;

Qy 447 GCTGCGCGGCTTCGCGCTTCCATCGACGCCGCGCGCTGCGCTTGAGTTTCG
 Dy 675 GCGCGCAAGGGCTCGCGAGGCCATCGAGCCGCTTACCGCGAGGGG
 Qy 507 ATGGTGTAGTAACGGCCAAGTCAGGGGATGATGTTGCTTCGCGCATGAG
 Dy 735 AGCCCGAGGCTGCGCTGAGCTGCGGAAACTGCGCGCTGCGCATGAG

Result No.	Score	Query Match Length	DB ID	Description
1	1407	100.0	12732	X Sequence 1, Applied
2	693	49.3	693	12 US-11-143-401-44 Sequence 44, Applied
3	427	30.3	427	12 US-11-143-401-43 Sequence 43, Applied
4	36.2	2.6	8116	8 US-10-995-661-13351 Sequence 13351, Applied
5	36.2	2.6	222094	8 US-10-995-561-13244 Sequence 13244, Applied
6	35.4	2.5	622	6 US-09-925-065A-597843 Sequence 597843, Applied
7	34.6	2.5	388	6 US-09-925-065A-585977 Sequence 585977, Applied
8	34.6	2.5	496	6 US-09-925-065A-827710 Sequence 827710, Applied
9	34.2	2.4	634	6 US-09-925-065A-311017 Sequence 311017, Applied
10	33.8	2.4	810	8 US-10-467-657-5805 Sequence 5805, Applied
11	33.6	2.4	535	6 US-09-925-065A-26675 Sequence 26675, Applied
12	33.4	2.4	388	6 US-09-925-065A-585978 Sequence 585978, Applied
13	33.4	2.4	613	6 US-09-925-065A-411236 Sequence 411236, Applied
14	33.4	2.4	1194	6 US-09-925-065A-279367 Sequence 279367, Applied
15	33.2	2.4	600	8 US-10-750-623-707 Sequence 707, Applied
16	33.2	2.4	600	8 US-10-750-623-707 Sequence 707, Applied
17	33	2.3	388	6 US-09-925-065A-585976 Sequence 585976, Applied
18	33	2.3	634	6 US-09-925-065A-311018 Sequence 311018, Applied
19	33	2.3	634	6 US-09-925-065A-311019 Sequence 311019, Applied
20	32.6	2.3	164810	12 US-11-121-086-4 Sequence 4, Applied

121	CATTAGCAGTGCCTGCGTCAGCTGATGTGGCACCAATTCTGGTCGAACGTTCA	180	Db	1201 ATCTTGTGATGAAAGCTCCCTTCAGCTGAGGGAAACAGTATCCACTGTAACCTGG	1262			
181	GACGAGCATTTGAAATTCCACTTGGAGCTTACTCCGCTCCGATCTATGGGGGG	240	Qy	1261 CTCGTTTGTGATCCGATTTCTGTTGCCAATTCAGCTGGTATATTGATCTGATCTAG	1320			
181	GACGAGCATTTGAAATTCCACTTGGAGCTTACTCCGCTCCGATCTATGGGGGG	240	Db	1261 CTCGTTTGTGATCCGATTTCTGTTGCCAATTCAGCTGGTATATTGATCTGATCTAG	1320			
241	CGCGATGAACTCTGCGTGCCTGCGAACCTTCGAAACGTTAGTGCCTGGCACCAATT	300	Qy	1321 ATGATGAACTCATCGAGAATGCAATCAGTCGAAATAATCCTCGCCAAAGGTATGTAATT	1380			
241	CGCGATGAACTCTGCGTGCCTGCGAACCTTCGAAACGTTAGTGCCTGGCACCAATT	300	Db	1321 ATGATGAACTCATCGAGAATGCAATCAGTCGAAATAATCCTCGCCAAAGGTATGTAATT	1380			
301	CGGGGAGAGCTGATGCGGTAAATCGTTTGAAAGCACTAGTGTCA	360	Qy	1381 GATGCAACATCGGCCACTTCTCAAC	1407			
301	CGGGGAGAGCTGATGCGGTAAATCGTTTGAAAGCACTAGTGTCA	360	Db	1381 GATTGAAACATCGGCCACTTCTCAAC	1407			
361	GTAGGCCCATAGGCCACAGCCTAGATCTGTGAAATAATGGCTCGGCCATTGACA	420	RESULT 2					
361	GTAGGCCCATAGGCCACAGCCTAGATCTGTGAAATAATGGCTCGGCCATTGACA	420	US-11-143-401-44-C					
421	TGCGCACCAGCTGGTCAAGCGCAACCGCTGCCCGCTTCCCATTCGAGCGCCC	480	Sequence 44, Application US-11-143401					
421	TGCGCACCAGCTGGTCAAGCGCAACCGCTGCCCGCTTCCCATTCGAGCGCCC	480	; Publication No. US2006002953A1					
481	GGGGTGTGGTTGCTGAGTTGATGGTTGAGTAACCGCCAACTGAGCGACCATGT	540	; GENERAL INFORMATION:					
481	GGGGTGTGGTTGCTGAGTTGATGGTTGAGTAACCGCCAACTGAGCGACCATGT	540	; APPLICANT: Behr, Marcel					
541	CGTTGCGTCTTCCCGCATGAGCTGCCCTCGAGATTGTGTGTGGCTGGTGTG	600	; APPLICANT: Small, Peter					
541	CGTTGCGTCTTCCCGCATGAGCTGCCCTCGAGATTGTGTGTGGCTGGTGTG	600	; APPLICANT: Schoolnik, Gary					
601	GTCCGAGACTATACTTCACAGTGTGATGCCAGGGCTGGCGGCAATGACCCAAA	660	; TITLE OF INVENTION: Molecular Differences Between Species of					
601	GTCCGAGACTATACTTCACAGTGTGATGCCAGGGCTGGCGGCAATGACCCAAA	660	; TITLE OF INVENTION: the M. Tuberculosis Complex					
661	CCCCCGGGACGGTTGGCGAGGAGGCTGGTGAAGCACTAATTCTACTGGCA	720	; CURRENT APPLICATION NUMBER: US/11/143, 401					
661	CCCCCGGGACGGTTGGCGAGGAGGCTGGTGAAGCACTAATTCTACTGGCA	720	; CURRENT FILING DATE: 2005-06-01					
721	CAGTACCTGAAATTACTCCGAGCTTCCGAGCTTAAAGAGCAGATCGAC	780	; PRIORITY APPLICATION NUMBER: US/10/647, 089					
721	CAGTACCTGAAATTACTCCGAGCTTCCGAGCTTAAAGAGCAGATCGAC	780	; PRIORITY FILING DATE: 2003-08-21					
781	ACGGGGGTCTGAACTCTCCACATTCTTAAATCGGTAGCCGTCATAATCGAC	840	; PRIORITY APPLICATION NUMBER: US/09/894, 844					
781	ACGGGGGTCTGAACTCTCCACATTCTTAAATCGGTAGCCGTCATAATCGAC	840	; PRIORITY FILING DATE: 2001-06-27					
841	CAAGTTACCGGATGCTAAGTCGCTGATCCGATGAGCTGATGAGCTGAG	900	; PRIORITY APPLICATION NUMBER: 09/318, 191					
841	CAAGTTACCGGATGCTAAGTCGCTGATCCGATGAGCTGATGAGCTGAG	900	; PRIORITY FILING DATE: 1999-05-25					
901	GGGCGAGAGACATATTCTGGCTGCTGGCTGCTGGCTCATGGCTCATGGCTG	960	; PRIORITY FILING DATE: 1998-08-25					
901	GGGCGAGAGACATATTCTGGCTGCTGGCTGCTGGCTCATGGCTCATGGCTG	960	; NUMBER OF SEQ ID NOS: 137					
961	TTGGCGTCCGGCTTAATTCTGGCTGCCAGTTGGCTGCTGATACCGAGATA	1020	; SOFTWARE: FastSeq for Windows Version 4.0					
961	TTGGCGTCCGGCTTAATTCTGGCTGCCAGTTGGCTGCTGATACCGAGATA	1020	; SEQ ID NO: 44					
1021	CTGCAAATTCGCAATTGATGAACTGCGCTCATGACATCGAAGCTGCTG	1080	; LENGTH: 693					
1021	CTGCAAATTCGCAATTGATGAACTGCGCTCATGACATCGAAGCTGCTG	1080	; TYPE: DNA					
1081	AGGTAAATCGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140	; ORGANISM: Mycobacteria tuberculosis					
1081	AGGTAAATCGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140	; LENGTH: 693					
1141	AATCTAGTCCGCCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200	; Query Match					
1141	AATCTAGTCCGCCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200	; Best Local Similarity					
1141	AATCTAGTCCGCCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200	; Matches 693; Conservative					
104	TTGGCGTCCGGCTTAATTCTGGCTGCCAGTTGGCTGCTGCTGCTGCTG	1080	; Score 693; DB 12; Length 693;					
104	TTGGCGTCCGGCTTAATTCTGGCTGCCAGTTGGCTGCTGCTGCTGCTG	1080	; Pred. No. 1.6e-211; Mismatches 0; Indels 0; Gaps 0;					
693	CTGGCGACAGTACCTGCTGGCTCCGAGCTTGGCTGCTGCTGCTGCTG	773	; Prior Filing Date: 2003-08-21					
693	CTGGCGACAGTACCTGCTGGCTCCGAGCTTGGCTGCTGCTGCTGCTG	773	; Prior Application Number: US/09/894, 844					
633	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	634	; Prior Filing Date: 2001-06-27					
633	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	634	; Prior Application Number: 09/318, 191					
774	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	833	; Prior Filing Date: 1999-05-25					
774	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	833	; Prior Application Number: 10/057, 936					
633	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	574	; Prior Filing Date: 1998-08-25					
633	AATCGAACACCGGGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	574	; Number of SEQ ID NOS: 137					
834	ATCGAACACCAAGTTACCGGGATGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	893	; Software: FastSeq for Windows Version 4.0					
573	ATCGAACACCAAGTTACCGGGATGCTGCTGGCTGACCCCTCCGAGCTAATTCTGGT	514	; SEQ ID NO: 44					
894	GGCTGAGGGCCAGGAGACAGACATATTCTGGCTGCTGGCTGCTGGCTGCTG	953	; LENGTH: 693					
513	GGCTGAGGGCCAGGAGACAGACATATTCTGGCTGCTGGCTGCTGGCTGCTG	454	; TYPE: DNA					
954	CTCGCTCTTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1013	; ORGANISM: Mycobacteria tuberculosis					
453	CTCGCTCTTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	394	; LENGTH: 693					
1014	GAGATAACTGCAAACTGCAATTGCAATTAATGCGCTGCTGCTGCTGCTG	1073	; Query Match					
393	GAGATAACTGCAAACTGCAATTGCAATTAATGCGCTGCTGCTGCTGCTG	334	; Best Local Similarity					
1201	ATCTTGTGATGAAAGCTCCCTTCAGCTGAGGGAAACAGTATCCACTGTAACCTGG	1260	; Matches 693; Conservative					

QY 1074 TTCTTCGACGTTAAATCGGGCGAGCCAGTCAGGATCTCGCAAAATGAGCAGCCGCCT 1133
Db 333 TTCTTCGAACTTAAATCGGGCGAGCCAGTCAGGATCTCGCAAAATGAGCAGCCGCCT 274

QY 1134 GTAGTTGAAATTCTAGTGCCTCGCCGAGTCGCTTTCGCCCATACTCGCTCGATCAGGT 1193
Db 273 GTAGTTGAAATTCTAGTGCCTCGCCGAGTCGCTTTCGCCCATACTCGCTCGATCAGGT 214

QY 1194 CTCAGTGAATCTTTGATGGAAAATCCCTTCACCTGGAGGGAAACAGTTATCAGTGA 1253
Db 213 CTCACTGTTCTCTTGATGGAAAATCCCTTCACCTGGAGGGAAACAGTTATCAGTGA 154

QY 1254 CCCCTGGCCTGGTTTGATCGAATTCTGTTTCGCAATTACGCTTGGATAATTGCAATC 1313
Db 153 CCCCTGGCCTGGTTTGATCGAATTCTGTTTCGCAATTACGCTTGGATAATTGCAATC 94

QY 1314 ATCATAGATGATGATTGAAATTCGAAATTATCAGTCAAATTATCCTCGCAAGGTA 1373
Db 93 ATCATAGATGATGATTGAAATTCGAAATTATCCTCGCAAGGTA 34

QY 1374 GAAATTGTTGAAATTCGACTTTCTCAA 1406
Db 33 GAAATTGTTGAAATTCGACTTTCTCAA 1

RESULT 3
US-11-143-401-43/C
Sequence 43, Application US/11143401
Publication No. US2006002953A1
GENERAL INFORMATION:
APPLICANT: Behr, Marcel
APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of
the M. Tuberculosis Complex
FILE REFERENCE: STAN102CON
CURRENT APPLICATION NUMBER: US/11/143,401
CURRENT FILING DATE: 2005-06-01
PRIOR APPLICATION NUMBER: US/10/647,089
PRIOR FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US/09/894,844
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US/09/318,191
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 498
TYPE: DNA
ORGANISM: Mycobacteria tuberculosis

US-11-143-401-43
Query Match Score 30.3%; DB 12; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.3e-126; Indels 0; Gaps 0;
Matches 427; Conservative 0; Mismatches 0;

QY 1 ACCCTGCGCTTGCAGAGATCAAATAGGGCGCATAGTAGCTGGTCAGCATGGCGCA 60
Db 427 ACCCTGCGCTTGCAGAGATCAAATAGGGCGCATAGTAGCTGGTCAGCATGGCGCA 368

QY 61 TCTTTGATGATCGGAATTAGATGTCAGGCAATTAAAGAGAAAGCCATGGCGCA 120
Db 367 TCTTTGATGATCGGAATTAGATGTCAGGCAATTAAAGAGAAAGCCATGGCGCA 308

QY 121 CATTCACTGATGTTGAGGCTCTGCTTGATGAGGACCATTCGGTCAAGGATTCA 180
Db 307 CATTCACTGATGTTGAGGCTCTGCTTGATGAGGACCATTCGGTCAAGGATTCA 248

QY 181 GAGGAACATGATGAAATTCACTGGAGGCTATAGTCGGCTCCGATCTATGCGGCCGG 240

Db 247 GACCAACATTGAAATTCCACTGGAGGCTATAGTCGGCTCCGATCTATGCGGCCGG 188
Db 241 CGCRGATGAGAGTCGTTGCGCCGACCTTCGAAAACCTAGTGGGCCGCCGACACATT 300
Db 187 CGAGATGAGAGTCGTTGCGCCGACCTTCGAAAAGTAGTGGGCCGCCGACACATT 128
Db 301 CGGGGAGAGCTGGTCAATCAGTTGGAGCCACCTAGTGAATGTCGA 360
Db 127 CGGGGAGAGCTGGTCAATCAGTTGGAGCCACCTAGTGAATGTCGA 68

QY 361 GTAGGCCCATAGCAGGCTAGATGTTGATCGAAAATGGTCCGCCGATTGACA 420
Db 67 GTAGGCCCATAGCAGGCTAGATGTTGATCGAAAATGGTCCGCCGATTGACA 8

Db 421 TGCGCAC 427
Db 7 TGCGCAC 1

RESULT 4
US-10-995-561-13351
Sequence 13351, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13351
LENGTH: 88116
TYPE: DNA
ORGANISM: Homo sapiens

US-10-995-561-13351
Query Match Score 2.6%; DB 8; Length 88116;
Best Local Similarity 62.9%; Pred. No. 3;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 403 GGTCGGCCCATGACATGCGACAGCTGGTCAAAGGCCTGGCCGCGCTTCGCG 462
Db 5737 GTCGGCCCATGACATGCGACAGCTGGTCAAAGGCCTGGCCGCGCTTCGCG 5796

Qy 463 CGTTCAATCGAGCCGGGGGTGGCT 491
Db 5797 CTCAAACCCCTTCGGCCAGGGCTT 5825

RESULT 5
US-10-995-561-13244/C
Sequence 13244, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13244
LENGTH: 22024
TYPE: DNA
ORGANISM: Homo sapiens

US-10-995-561-13244
Query Match Score 2.6%; DB 8; Length 222094;

RESULT 6
 US-09-925-065A-597843/c
 Sequence 597843, Application US/09925065A
 Publication No. US20040181048A1
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.115
 CURRENT APPLICATION NUMBER: US/09/925-065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 597843
 LENGTH: 622
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-597843

Query Match 2.5%; Score 35.4; DB 6; Length 622;
 Best Local Similarity 49.7%; Pred. No. 0..73; Indels 91; Gaps 0;
 Matches 90; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1202 TCTTTGATGGAAACGTCCCTACCGTGAAGTATCCACTGTAACTGC 1261
 Db 619 TCTGGGCTACAGCAGCTCCACCTTAGCCCTCTGAGTGCACTATGCTGAC 560
 Qy 1262 TCCTTTGTATCCGATTCGTTICGCCATACAGCTTGTATTGCAATGATA 1321
 Db 559 TAATGTTAAATTTTTTTTGAAACAGATCTCCATGTTGCCAGGGTGA 500
 Qy 1322 TGATGAATTCAIGACGATGAAATCAGGTCAAATATCCTGGCAAGGTATGTAATTG 1381
 Db 499 TTCAAAATTCTGGGTCAAGGAAATCCTCCACCTTAAGTGTGGGATTAG 440
 Qy 1382 A 1382
 Db 439 A 439

PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8227710
 LENGTH: 496
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-8227710

RESULT 7
 US-09-925-065A-585977
 Sequence 585977, Application US/09925065A
 Publication No. US20040181048A1
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925-065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8227710
 LENGTH: 496
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-8227710

Query Match 2.5%; Score 34.6; DB 6; Length 496;
 Best Local Similarity 53.3%; Pred. No. 1..2; Mismatches 64; Indels 0; Gaps 0;

Qy 1209 ATGGAAACGTCCCTCACCTGGAAACGTATCCACTGTTAACCTGACTCTGTT 1268
 Db 89 ATAAGGAGGTAACTTCTGCTGAAAGAAAGTACCATCTCTGTTCATGATPAT 148
 Qy 1269 GATCCGATTCTGTTGCCAATCAAGCTTGSTATATTGCAATGATGAA 1328

RESULT 9
US-09-925-065A-311017/c
; Sequence 311017, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FABSEQ for Windows Version 4.0
; SEQ ID NO: 311017
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-311017

Query Match 2.4%; Score 33.9; DB 8; Length 810;
Best Local Similarity 51.7%; Pred. No. 2.7;
Matches 77; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
; TYP: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5805

Query Match 2.4%; Score 33.9; DB 8; Length 810;
Best Local Similarity 51.7%; Pred. No. 2.7;
Matches 77; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
; TYP: DNA
; ORGANISM: Neisseria gonorrhoeae

Qy 191 GAATATCCACTCGGACGTATAGTCGGCTCCGATCATGGCGCCGAGTGAA 250
Db 21 GAAATTCCGTCGTTGATGTTGAGGAACTGGTCACTGGT 80

Qy 251 GTCTCGGTTGCCAACCTTCGAACAGTACTGGCCGGGAGAC 310
Db 81 GTATGGTTGACGACGGGAGATATGGGAAGGGACTATGGCTGAAGC 140

Qy 311 GTCGATGCCGTTGATACTGTTTGAAGC 339
Db 141 CAGGTTGTCGGGGTGCAGGGCTTCGGC 169

RESULT 11
US-09-925-065A-268665
; Sequence 268675, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 268675
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-268665

Query Match 2.4%; Score 33.6; DB 6; Length 535;
Best Local Similarity 57.7%; Pred. No. 2.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
; TYP: DNA
; ORGANISM: Homo sapiens

Qy 1291 TCAGCTTGGTATTCGATCATAGTAGTAACTCATCGAAGATGCAATCAGG 1350
Db 350 TCATTCTCTTACTCATCTAACTCATCGTGGAAACCGGGAAAATGCACTCAGG 409

Qy 1351 TCATAATTCCTCCAACTGATATGTTGATGACATCGC 1394
Db 410 GCATATCATATTGCTCAGAATGTATTCCTGCAAACCTGGC 453

RESULT 12
US-09-925-065A-585978
; Sequence 585978, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: SeqWIn99, version 1.04
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SEQ ID NO: 5805

; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine NMBT09508
US-10-750-185-707

Query Match 2.4%; Score 33.2; DB 8; Length 600;
Best Local Similarity 61.6%; Pred. No. 3.7;
Matches 33; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 1298 TGGPATATGCGATCTCATAGTAGTGATAATTICATCGAAGATGCCATCAGTCAAAAT 1357
Db 139 TGGATTTCGCACTAGTTAAACATTATCTTGACTATGGCATAGGAAAT 198
Qy 1358 ATCCCTCGCCAGGTATGTTATTGAT 1383
Db 199 ATACCCTGGAAAGATGTGAATTAAAT 224

Search completed: February 20, 2006, 02:42:19
Job time : 461.429 secs

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